

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 142881

TO: Jeffrey Parkin

Location: REM 3d39 / 3c18

Art Unit: 1648

Tuesday, January 25, 2005

Case Serial Number: 09/319156

From: Deirdre Arnold

Location: Biotech-Chem Library

REM 1A64

Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

Please contact me if you need to search the pending files.

Please contact me if you encounter any problems with the file or the disk.

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards, Deirdre Arnold



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STIC-Biotech/ChemLib

142354 142881

From:

Parkin, Jeffrey

Sent:

Tuesday, January 11, 2005 8:50 PM

To:

STIC-Biotech/ChemLib

Subject:

SEQUENCE SEARCH: U.S. Serial No. 09/319,156

Please search **SEQ ID NOS.:** 6, 9, 10, and 12 from the aforementioned application (U.S. Serial No. 09/319,156) v. all relevant databases.

Please provide the first 30 SUMMARIES.

Place results on both paper and disk.

Thanks!

JSP AU 1648 REM-3D39 2-0908

http://expoweb1:8001/cgi-bin/expo/GenInfo/snguery.pl?APPL_ID=09319156.

STAFF USE ONLY

Searcher: Application Searcher Phone: 2-2530 Date Searcher Picked up: 11900

Date Completed:

Searcher Prep/Rev. Time: Online Time:

Type of Search
NA Sequence: #_______
AA Sequence : #______
Structure: #______
Bibliographic:______
Litigation:_____
Patent Family:______
Other:

Vendors and cost where applicable STN:_______
DIALOG:_______
QUESTEL/ORBIT:_______
LEXIS/NEXIS:______
SEQUENCE SYSTEM:______

WWW/Internet:_

Other(Specify):

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model Run on:

January 22, 2005, 10:09:14; Search time 2663.68 Seconds (without alignments) 11273.477 Million cell updates/sec

Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters:

4526729 seqs, 23644849745 residues

Searched:

9053458

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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99 bhtg: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AR344385 Sequence AX001024 Sequence BD136195 Retrovira AF127229 Multiple AC113137 Homo sapi AC013346 Homo sapi	AC022171 Homo sapi AC010778 Homo sapi AL162912 Human DNA AC073626 Homo sapi	
SUMMARIES	AR344385 AX001024 BD136195 AF127229 AC113137 AC019346	AC022171 AC010778 AL162912 AC073626	ACO68898 AL583805 ACO72023 BSO00045 APO01574 APO01574 ACO90313 ACO90313
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% Query Match	100.0 100.0 100.0 100.0 99.5	99.5 91.4 91.2 9.6	8888.2.2.8.8.8.9.2.9.8.8.8.9.9.9.9.9.9.9
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ALIGNMENTS

mRNA linear PAT 17-AUG-2003 703.	Unknown. Unknown. Unclassified. Unclassified. Unclassified. Ferron,H., Beseme,F., Bedin,F., Paranhos-Baccala,G., Komurian-Pradal,F., Jolivet-Reprand,C. and Mandrand,B. Komurian-Pradal,F., Jolivet-Reprand,C. and Mandrand,B. Isolated nucleotide sequences associated with multiple sclerosis or rheumatoid arthritis and a process of detecting rheumatoid arthritis and a process of detecting Location/Qualifiers 1. 635 /organism="unknown" /mol_type="mRNA"	, DB 6, Length 635; 1.1e-189; nes 0; Indels 0; Gaps 0;	CCCIGIAICTITAACCICCTIGITAAGITIGICICTICCAGAAICAAAACIGAAACIA 60 	CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120 	CTGGACCGGCCTGCTAGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG 180 	GADATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT 240
635 bp US 6582703	Bedin, F., Paranh Livet Reynaud, C. quences associals nd a process of 02 24-UUN-2003; ifiers known"	Score 635; Pred. No. 1. Mismatches	TAAGTTT TAAGTTT	CCAGATG CCAGATG	CTCCGATC CTCCGATC	ACTATGC(ACTATGC
from patent .I:33740326	ied. 1 to 635) Beseme,F., Bedin, Fradel,F., Jolivet- mucleotide sequence d arthritis and a p 6 582703-A 102 24-8 Location/Qualifiers 1. 635 /organism="unknown"	.0%; Sc .0%; Pr	TAACCTCCTTGT] 	TCAAATGGAGCAC 	TGCTAGCCCATGC	TGCACAACCCT7
AR344385 Sequence 102 AR344385 AR344385.1 G	Unknown. Unknown. Unclassified. Unclassified. Unclassified. Perron,H., Beseme,F. Gonurian-Pradel,F., Isolated nucleotide rheumatoid arthritis Patent: US 582703-2 I. GSS /organism='/mol_type='/mol_ty	ch 1 Similarity 100 635; Conservative				
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RESULT 1 AR344385 LOCUS DEFINITION ACCESSION VERSION	ACT WORDS SOURCE ORGANIS REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUR	Query Ma Best Loc Matches	දු පු	λ β	% a	è q

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TE (bases 1 to 635)

Baccala,G.P., Pradel,F.K., Bedin,F., Sodoyer,M., Ott,C., Mallet,F., Perron,H. and Mandrand,B.

Perron,H. and Mandrand,B.

Retrovival nucleic material and nucleotide fragments, in particular, associated with multiple sclerosis and/or rheumatoid arthritis, for diagnostic, prophylactic and therapeutic uses

BIO MERIEUX

OS Unidentified

PN JP 2002509437-A 5 26-MAR-2002;

PN JP 2002509437-A/5

PD 26-MAR-2002

PR J-10-1998 JP 1999508255

PR 07-JUL-1997 FR 97/08816

PI GIAUCIA PARAHNOS BACCALA, FLORENCE KOMURIAN PRADEL, FREDERIC PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BD136195 635 bp DNA linear PAT 18-SEP-20 Retroviral nucleic material and nucleotide fragments, in particular, associated with multiple sclerosis and/or rheumatoid architis, for diagnostic, prophylactic and therapeutic uses.
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Ott, C. and Bedin, F.
RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR
RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR
ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR
DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES
PATENT: WO 9902666-A 6 21-JAN-1999;
BIO MERIBUX (FR); OTT CATHERINE (FR)
Location/Qualifiers
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                                                                       AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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/mol_type="unassigned DNA"
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2 (bases 1 to 2004)
XComurian-Pradel,F., Paranhos-Baccala,G., Bedin,F.,
Ounanian-Pradel,F., Paranhos-Baccala,G., Rajoharison,A., Garcia,E.,
Maller,F., Mandrand,B. and Perron,H.
Direct Submission
Submitted (10-F899) UMR103 CNRS, bioMerieux, 46, allee
D'Italie, Lyon 65007, France
Location/Qualifiers
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    .2004
/organism="Multiple sclerosis associated retrovirus

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    .2004
/note="similar to pol-env and 3'LTR

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100.0%; Pred. No. 1.3e-189;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:89382"
/clone="CL6"
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 635; Conservative
                                                                                                                                                                                                                           element"
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ACCESSION
VERSION
    REFERENCE
AUTHORS
                                                                                         TITLE
JOURNAL
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Multiple sclerosis associated retrovirus element clone CL6
pol-env/3'LTR-11ke mRNA sequence.
AF127229.1 GI:5726294
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Wintiple sclerosis associated retrovirus element
Viruses; Retroid viruses; Retroviridae.
1 (bases 1 to 2004)
Komurian-Pradel,F., Paranhos-Baccala,G., Bedin,F.,
Ounanian-Praza,A., Sodoyer,M., Ott,C., Rajoharison,A., Garcia,E.,
Mallet,F., Mandrand,B. and Perron,H.
Molecular cloning and characterization of MSRV-related sequences
associated with retrovirus-like particles
Virology 260 (1), 1-9 (1999)
                                                                                                                                                                                                       CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                              CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
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                                                                                         100.0%; Score 635; DB 6; I
100.0%; Pred. No. 1.1e-189;
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                                                                                                                                    0; Mismatches
  /mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                  Matches 635; Conservative
                                                                                                                Best Local Similarity
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RESULT 4 AF127229 LOCUS DEFINITION

VERSION KEYWORDS SOURCE ORGANISM ACCESSION

REFERENCE AUTHORS

TITLE

PUBMED JOURNAL

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McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.
Trauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                               Submitted (155-ARR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAY 22, 2002 this sequence version replaced gi:18875226. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI-11 Human Male BAC"
2566. .2593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seg.wi.mit.edu
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complement(8444. .8971)
/rpt family="LiM534"
complement'
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complement(9387, 9600)
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9898. .10497

    167694
    organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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6723. .6750
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6982_.7280
/rpt_family="Alux"
7780_.7281
/rpt_family="AT_rich"
/rpt_family="AT_rich"
complement(8120_.8302)
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complement(12442..13
/rpt_family="L1PA16"
13550..13907
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5234. .6028
/rpt_family="LimE3"
complement (6259. .647
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3. .11555
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4840. .5079
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                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 18, clone RP11-622J9
                                                                                                                                                                                                                                                                                 (bases 1 to 167694)
                                                                                                                                                                 (bases 1 to 167694)
                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                 Unpublished
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Homo sapiens chromosome 18 clone RP11-497M7 map 18, WORKING DRAFT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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                                                            AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
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25154. :25156
    // note="single clone coverage"
25189. :25193
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    // complement(26144. :26248)
    // rpt femily="MIR"
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31912. .31989
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/rpt_family="LIMB3"
complement(20633. .22006)
/rpt_family="LIP"
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complement(32304. .34133)
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24420. .24468
/rpt_family="AT_rich"
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24886. .24913 /
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29367. .29451
/rpt_family="GA-rich"
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                                               /rpt_famlly_
15633. 15912
/rpt_family="(TA)n"
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15920. .16279
/rpt_family="L1PB1"
16338. .17100
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32017. .32303
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7572. .17628
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AC022171 21-00136 bp DNA linear HTG 26-MAR-2001 Homo sapiens chromosome 18 clone RP11-407C18, WORKING DRAFT SEQUENCE, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 210336)

Abola,A.P. Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R., Mao,J., Komp,C., Kottler,S., Lam,B., Marathe,R., Miranda,M., Morehouse,A.J., Webb,C., Wilhelmy,J., Palm,C.J., Ramirez,D., Southwick,A.M., Webb,C., Wilhelmy,J., Yu,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-JAN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ Genome Center
Center: Stanford DNA Sequencing and Technology Development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reads
                                                                                                                                       541 CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTCACTCTATTTCACTCT
481 AGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         To Chases 1 to 210336)
Bruno, D., Conn, L., Dela Rosa, M., Federspiel, N., Foreman, P., Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Vis. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing Vector: plasmid, X02513; 97% of reads Sequencing Vector: plasmid, plasmid_accession, 3% of read Chemistry: Dye-ptimer; 10% of reads Chemistry: Dye-terminator Blag Dye; 88% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 208312 bases at least Q40 Consensus quality: 208312 bases at least Q40 Consensus quality: 208312 bases at least Q20 Consensus quality: 209157 bases at least Q20 Insert size: 199762; agarose-fp Insert size: 199762; agarose-fp Insert size: 210236; sun-of-contigs Quality coverage: 8.7x in Q20 bases; sum-of-contigs.

* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pleces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Mar 10, 2001 this sequence version replaced gi:13122770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC022171
GC0221711.18 GI:13270574
HTG; HTGS PHASEL; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                    149924 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAAAAA 149890
                                                                                                                                                                                                                            601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAA 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: 758
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VERSION
KEYWORDS
SOURCE
ORGANISM
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
AC022171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150224 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 150165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150164 GCATICCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGGACCAATCAGAGAGCTC 150105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCAGCCAACCTCCCCAACAGAGACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                         Sequencing vector: M13; M77815; 32% of reads
Sequencing vector: Plasmid; n/a: 68% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap, version 0.960731
Consensus quality: 176087 bases at least Q40
Consensus quality: 176085 bases at least Q20
Consensus quality: 176095 bases at least Q20
Insert size: 178000; agarose-fp
Insert size: 178000; agarose-fp
Insert size: 176095; sum-of-contigs
Quality coverage: 11.5 in Q20 bases; agarose-fp
Quality coverage: 11.7 in Q20
* NOTE: This is a "working draft' sequence. It currently
* consists of I contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

I 176095: contig of 176095 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="18"
/map="18"
/mol="18"
/clone="18"
/clone="lb="RPI1-497M7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 631.8; DB 2;
Pred. No. 2.9e-188;
0; Mismatches 2;
     ----- Project Information
                                                          er clone name: 497 M 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                Center project name:
Center clone name: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.5%;
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Best Local Similarity
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Collymore, A., Castle, A., Collymore, A., Cooke, P., DeArellano, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Haeford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnor, P., Peterson, K., Pollara, V., Rilay, R., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Nayman, D., Ye, W.J., Zimmer, A. and Zody, M.

Lubmitted (12-SBP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On Mar 30, 2000 this sequence version replaced gi:6087973.

All repeats were identified using RepeatMasker: html

Conter: Whitchead Institute/ MIT Center for Genome Center. Genome Center.
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 148724)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 182000; agarose-fp
Insert size: 148024; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 4.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2462: contig of 2462 bp in length
2562: gap of 100 bp
7944: contig of 5386 bp in length
8048: gap of 100 bp
15800: contig of 7752 bp in length
15500: gap of 100 bp
25559: contig of 9159 bp in length
25159: gap of 100 bp
41906: contig of 16747 bp in length
42006: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence submissions@genome.wi.mit.edu
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of 35146 bp in length
                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-2N15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
Web Bite: http://www-seg.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: 12677
  AC010778.3 GI:7341824
HTG; HTGS PHASE1; HTGS DRAFT.
HOWO sapiens (human)
Howo sapiens
                                                                                                                                                                                                                                                             (bases 1 to 148724)
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63441:
98587:
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Homo sapiens clone RP11-2N15, WORKING DRAFT SEQUENCE, 8 unordered
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  66568: gap of unknown length 210336: contig of 143768 bp in length.
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/chromosome="18"
/clone="RP11-407C18"
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                                                                                                                                                                                                                                                                                             1. .66468
/note="assembly_name:Contig44
                                                     Location/Qualifiers
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AC010778/c DEFINITION ACCESSION

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8 98687: gap of 100 bp
8 148724: contig of 50037 bp in length.
Location/Qualifiers
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                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
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/clone="RP11-2N15"
/clone="RP11-115"
                                                                                                                                                                                                                                                                                                                                                                                                        91.4%; Score 580.2; DB 2; 94.8%; Pred. No. 6.7e-172; iive 0; Mismatches 33;
                                                                                                                       25160. .41906 // note="assembly_fragment" 42007. .63341 // note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                         63442. .98587
/note="assembly_fragment"
98688. .148724
/note="assembly_fragment"
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/note="assembly_fragment"
                                                                                                                                                                                  8049. .15800
/note="assembly_fragment
                                                                                                                                                                                                                        vector_side:right"
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Direct Submitted

Cambridgeshire, CB10 184, UK. E-mail enquiries.

Cambridgeshire, CB10 184, UK. E-mail enquiries.

Cambridgeshire, CB10 184, UK. E-mail enquiries.

Lumming sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em; EMBL; Swi. SMISSPROT; Tri. TREMBL; Wp.; WORNDEP; Information

on the WORNDEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome X, constructed by the Sanger Centre Chromosome X Mapping

Group. Further information can be found at

this sequence was finished as follows unless otherwise noted: all

regions were either double-etranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

sasembly was contirmed by restriction digest. RP6-198C4 is from the

library RPGI-6 constructed by the group of Pieter de Jong. For

further details see

http://www.space.
                                                                                                                             Human DNA sequence from clone RP6-198C4 on chromosome Xq13.3-21.2, complete sequence.
ALI62912 ALI21824
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 8339)
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/note="HERV17 repeat: matches 7419. 7457 of consensus"
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/note="HERV17 repeat: matches 8244. .8523 of consensus"
5956. .6136
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39671 ATTAAATCTTGCAACTGAAAAAAAAAAATGCAA 39639
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Loases I to 136901)

Hillier, M. Fulton, R.S., Fulton, L.A., Graves, T.A., Pepin, K.H., Wagner-McPherson, C., Layman, D., Maas, J., Jaeger, S., Walker, R., Wagner-McPherson, C., Layman, D., Maughin, M.D., Schaller, M.E., Fewell, G.A., Delehaunty, K.D., Miner T.L., Nash, W.E., Cordes, M., Du, H., Sun, H., Edwards, J., Bradshaw-Cordum, H., Ali, J., Andrews, S., Isak, A., Vanbruut, A., Nguyen, C., Du, F., Lamar, B., Courtney, L., Kalicki, J., Ozersky, P., Bielicki, L., Scott, K., Holmes, A., Karlow, A., Stong, C.M., Hou, S., Tomlinson, C., Dauphin-Kohlberg, S., Kozlowicz-Reilly, A., Leonard, S., Rohlfing, T., Strowmatt, C., Latreille, P., Miller, N., Johnson, D., Murray, J., Woessner, J.P., Wendl, M.C., Yang, S.P., Schultz, B.R., Wallis, J.W.,
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                                                                                                                                                  CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
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                                                                                                                                                                                                                                                                                                   GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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                                                                           CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCTTCCAGAATCAAAACTA
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                                      Gaps
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Homo sapiens BAC clone RP11-95P9 from 7, complete sequence.
ACU/3626
                                    ó
 Length 8339;
                                    Indels
                                    33;
DB 9;
Score 579.2; DB 9;
Pred. No. 8.4e-172;
0; Mismatches 33;
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91.2%;
94.8%;
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                                  Matches 599; Conservative
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                     Best Local Similarity
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Query Match
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Direct Submission
Submitted (O9-MXY-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
(Chases 1 to 136901)
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Submitted (27-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
M 63108, USA
4 (Dases 1 to 136901)
Waterston, R.H.
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Submitted (16-FEB-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
School of Medicine, 4444 Forest Park Parkway, St. Louis,
Schoses 1 to 136901)
Spieth, J., Bieri, T.A., Nelson, J.O., Berkowicz, N., Wohldmann, P.E., Cook, Li., Hickenbotham, M.T., Eldred, J., Williams, D., Bedell, J.A., Mardis, E.R., Clifton, S.W., Chissoe, S.L., Marra, M.A., Raymond, C., Haugen, E., Gillett, W., Zhou, Y., James, R., Phelps, K., Iadanon, C., Bubb, K., Simms, E., Levy, R., Clendenning, J., Kaul, R., Kent, W.J., Furey, T.S., Baertsch, R.A., Brent, M.R., Keibler, E., Flick, P., Chinwalla, A.T., Gish, W.R., Eddy, S.R., McPherson, J.D., Chinwalla, A.T., Gish, W.R., Eddy, S.R., McPherson, J.D., Olson, W.V., Eichler, E.E., Green, E.D., Waterston, R.H., and Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (29-APR-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
7 (bases 1 to 136901)
Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63108,
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Submitted (30-JAN-2004) Department of Genetics, Washington
University, 444 Forest Park Avenue, St. Louis, Missouri 63
On Peb 16, 2001 this sequence version replaced gi:11597125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 136901)
Bauer, H., Haakenson, B. and Nguyen, C.
The sequence of Homo sapiens BAC clone RP11-95P9
Unpublished (2001)
3 (bases 1 to 136901)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                         Nature 424 (6945), 157-164 (2003)
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NOTICE: This sequence may not represent the entire insert of this fone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Contact: sapiens@watson.wustl.edu site: http://genome.wustl.edu Center project name: H_NH0095P09 This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information

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95258
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Pred. No. 5.4e-169;
0; Mismatches 40; Indels 0;
                                                                                                                                                         /rpt family="AT rich"
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15255. .15456
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22576. .23085
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23097. .24931
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18604. .19120
/rpt_family="MaLR"
20362. .20667
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6497, .16517
                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Alu"
20943. .20966
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Best Local Similarity 93.7%;
Matches 595; Conservative
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                                                                                                                                                                                                                                         The clone sequenced to the left is CTD-2023N18, 200 bp overlap the clone sequenced to the right is CTA-250D13, 200 bp overlap. Actual start of this clone is at base position 127066 of CTD-2023N18 actual end is at base position 26937 of CTA-250D13.
                                                                           The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and Coworkers at http://www.chori.org
                     http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send
mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu
      about the map position of this sequence, see
                                                                                                                                                                                                                               NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                             1. .136901
/organism="Homo sapiens"
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412. 9494
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3118. .3324
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14396. 14434
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10815. 10909
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786. .7823
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433. .7770
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1533. .1790
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2972. .3112
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Homo sapiens chromosome 10 clone RP11-534L6, complete sequence.
ACO68898
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176188)
Smith, D.R.
                                                                                                                                                                                                                                                                                                      Genome Therapeutics Corporation Sequencing Center: Human Genome
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Submitted (29-AUG-2002) Genome Therapeutics Corporation, 100
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On Aug 29, 2002 this sequence version replaced gi:14625082.
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                                                   Score 566.4; DB 9
Pred. No. 1.6e-167
0; Mismatches 41
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/clone="RP11-534L6"
/clone_lib="RPCI-11"
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Smith, D.R.
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Best Local Similarity 93.5%;
Matches 591; Conservative (
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All Submitted (29-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Blirect Submitted (29-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (29-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CENO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk on Oct 2, 2001 this sequence version replaced gi:14702155.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotations corresponding to the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by a constructed by all regions were covered by as compressions are used to resolve all sequencing problems, such as compressions are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; Wp:, WORWEPP; Information on the WORWPEP database can be found at the contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 mapping Group. Purcher information can be found at the proup of Pieter de Jong. For further details see the contigs of human chroming and replace and the prompt of Pieter de Jong. For further details see the contigned by the sanger human the contribution of the proup of Pieter de Jong. For further details see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL583805 89728 bp DNA linear PRI 29-SEP-2001
Human DNA sequence from clone RP11-134K1 on chromosome 9, complete
sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAGCACAGTGGGGACGACAAGGATTGCAATATAAACCCAGGCATTCGAGCCAGCAACGG
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                                                                                                                                                                                                                                                     AGAGCACACGCGCGCACAAGGATCGGCATATAAACCCAGGCATTCGAGCCCGCCAACGC
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                                                                                 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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VBCTOR: pBACe3.6
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AL583805.7 GI:15865009
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Alebrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Burbrais, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bovie, S., Brieva, M., Brown, B., Brown, M., Eryant, N. P., Buhay, C., Burach, P. C., Burach, R. L., Byrd, N. C., Carron, T. C., Eurer, M., Cavacos, S. R., Charko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Dathorne, S. R., David, R., Davila, M. L., David, R., Dalayla, M. L., David, R., Delancy, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Dugan-Rochas, S. Durbin, K. J., Barnhart, C., Edgar, D., Edwards, C. C., Elbaj, C., Escetto, M., Falls, T., Ferraguto, D., Edwards, C. C., Elbaj, C., Bacchto, M., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, M., Havlak, P., Hale, S., Hamilton, K. Harris, C., Harris, R., Harris, T., Harris, R., Harris, R., Harris, R., Harris, R., Harris, R., Warthor, D., Kueseh, J., Hollins, B., Homei, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Martinez, C., Liu, J., Liu, Z., Lidchtarge, O., Lieu, C., Liu, J., Liu, R., Martinez, R., Massey, E., Mawhiney, E., Mclean, R., Martinez, R., Massey, E., Mawhiney, E., Mclean, R., Martinez, R., Massey, E., Mawhiney, E., Mclean, R., Neterson, B., Newtson, M., Notrien, R., Newtson, N., Sisson, I., Sodergren, Sonaike, T., Sparke, A., Paner, P., Tameris, A., Tameri, M., Taney, J., Tameris, A., Tameri, M., Warten, Y., Villalon, D., Vinedon, S., Wolled, S., Wolled, S.,
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Worley, K.C.
Direct Submission
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Homo sapiens 3 BAC RP11-3J2 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 112405)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   83434 cccrcraraterriaaccrccrraraagrararcrcrrccagaarcgaagcraraa---ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83511 GAAATCTCAACTGCACAACAACTACTATGCCCCCAATTCAGCAGGAAGCAGTTAGAGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                               1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GABATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                        34; Indels 3;
                                                                                                                                                                                                                                                                                         Length 89728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84031 ATTAAATCCTGCAACTGCAAAAAAAAAAAAAAAA 84065
                                                                                                                                                                                                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAAAA 635
                                                                                                                                                                                                                                                                                         Score 564.6; DB 9
Pred. No. 5.4e-167,
0; Mismatches 34
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chromosome="9"
/clone="RR11"
/clone="RR11"
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AC072023.9 GI:27764634
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.2%;
Matches 598; Conservative
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AC072023
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Gibbs, k.
Direct Submission
Unpublished
2 (bases 1 to 112405)
Worley, K.C.
Direct Submission
Submitted (07-UTM-2000) Human Genome Sequencing Center, Department
Submitted (07-UTM-2000) Human Genetics, Baylor College of Medicine, One Journal Morley, K.C.
Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department Submitted (Molecular and Human Genetics, Baylor College of Medicine, One Direct Submission Submitted (22-UTN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 112405) Submitted (16-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, 77030, USA On Jan 16, 2003 this sequence version replaced gi:21539113. Submitted (30-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                               CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Peatures listing.
                                                                                                                                                                                                                                                                                                  ANDIATION OF FEMILIES.

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Muc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes adminarity (expect < 1e-34) to the EST and cDNA sequences identified shifts that maintained sequence continuity across the splice intocions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at URL:
http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of basety are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="overlaps bases 38072. .40071 of clone AC125608"
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu
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complement(1. .261)
/rpt_family="LiM4"
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/db_xref="taxon:9606"
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/rpt_family="LIMB"
complement (914, .1221)
/rpt_family="AluSg"
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4714. .4913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt family="Allos
complement (1222. .1808)
/rpt family="LIME"
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/rpt family="AT rich"
complement(6337. .6630)
/rpt_family="AluSx"
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/rpt_family="LIME"
2454. .2811
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complement (429777...467
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5632. .5670
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2813. .3092
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1947_3870
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1871. .3891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotation as Low Coverage.
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67581 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAATGGTAAAACTA 67640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGGTGGGAAGGTGACT
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Pred. No. 1.4e-165;
0; Mismatches 38;
                                               Complement (7934.7)

Complement (7936. 7695)

/ppt family="Alusx"

7910. 8035

/rpt family="MIR"

8824. 10387

/rpt family="MIR"

10388. 10412

/rpt family="AT_rich"

10637. 10675

/rpt family="AT_rich"

/rpt family="AT_rich"
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14620. .14933
complement(15183. .15254)
/rpt_family="Lys" 1.5.7
/rpt_family="Lys" 1.7.75
/rpt_family="Lys" 1.7.75
/rpt_family="Lys" 1.7.75
/rpt_family="Lys" 1.7.75
/rpt_family="Lys" 1.7.75
/rpt_family="Lys" 1.7.75
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complement(12819. .13533)
/rpt_family="L1"
13599. .13619
                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="L2"
complement(12489. .12812)
              /rpt_family="(TTTA)n"
complement(7094. .7374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family="AT_rich"
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[8793. .19462
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19461. .20130
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                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="L1"
11295. .11658
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93.8%;
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Best Local Similarity 93.8
Matches 594; Conservative
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http://www.chori.org/bacpac/mchimp43.htm.
The clone may be obtained from Pieter J. de Jong and coworkers
The clone may be obtained from Pieter J. de Jong and coworkers
(http://www.chori.org/bacpac).
VECTOR: pBACe3.6
The CHORI-231 chimpanzee BAC library was prepared from DNA isolated
from the blood of a single male chimpanzee using published
protocols (Oscagawa, F. et al. Genomics 52:1-8). The DNA from the
chimpanzee ('Clint') was obtained from the Yerkes Primate Center in
Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu,
Kazutoyo Oscagawa, Evan Eichler & Pieter J de Jong. The library
characteristics are described at
http://www.chori.org/bacpac/chimpanzee251.htm.
The clone may be obtained from Pieter J de Jong and coworkers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.chori.org/bacpac).
VBCTOR: pTARBAC2.1
The PTB1 chimpanzee BAC library was prepared from DNA isolated from
cultured cells established from the blood of a single male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clones may be obtained from Asao Fujiyama and co-workers (http://www.gsc.riken.go.jp).

RETOR: pxS145
The PTF22 chimpanzee Fosmid library was prepared from DNA isolated from cultured cells established from the blood of a single male
                                                                                                                                                                                                                                                                            The RPCI-43 chimpanzee BAC library was prepared from DNA isolated from the blood of a single male chimpanzee using published protocols (Osoegawa, K. et al. Genomics 52:1-8). The DNA from the chimpanzee ('Cilnit') was obtained from the Yerkes Primate Center i Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu, Kazutoyo Osoegawa, Evan Eichler & Pieter J de Jong. The library characteristics are described at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Quality Assessment:
This entry has been annotated with sequence
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in
                                9
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                        an attempt was made to resolve all sequencing problems, such compressions and repeats; all regions were covered by at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neighboring clones: RP43-014B20(left) and PTB-042H12(right).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.2%; Score 559.8; DB 9; Length 179114; ilarity 94.0%; Pred. No. 2e-165; Conservative 0; Mismatches 37; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones may be obtained from Asao Fujiyama and co-workers
                                                                                                                                        subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="pan troglodytes"
/mol_type="genomic DNA"
/db_xref="texon:9598"
/chomesome="12"
/clone="RP43-179P23"
/clone="RP43-179P23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.gsc.riken.go.jp).
VECTOR: pKS143
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                                                                                                                                                                                                                                                                    Source information:
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Best Local Simi.
Matches 582, (
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DNA sequence and comparative analysis of chimpanzee chromosome 22

In Nature 429, 382-388 (2004)

E 2 (bases 1 to 179114)

E 3 (bases 1 to 179114)

E 4 Hattori,M., Toyoda,A., Watanabe,H., Taylor,T.D., Kuroki,Y.,

Fujiyama,A. and Sakaki,Y.

Direct Submission

L Submitted (12-MAY-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

Tolishiattoriogsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Tel:81-45-503-9111, Fax:81-45-503-9170

Tel:81
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Contact: hattori@gsc.riken.go.jp
------- Project Information
Center project name:The Chimpanzee Chromosome 22 Sequencing Project
Center clone name: RP43-179P23
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                                                                                                                                                                                                                                    540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BS000045 179114 bp DNA linear PRI 12-JUN-200
Pan troglodytes chromosome 22 clone:RP43-179P23, map 22, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: pUC18,pUC13,pTZ19R; 100% of reads Chemistry: Dye-terminator Big Dye and ET; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 178,810 bases at least Q40 Consensus quality: 263 bases at least Q30
                                                                                                                421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATTGCCTG
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                                                                                                                                                                                                                                481 AGAGCACAGCGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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                                                                                                                                                                                                                                                                                                                                                                                     CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
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Center code: RIKEN
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AUTHORS
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JOURNAL
REFERENCE
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JOURNAL
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SOURCE
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RESULT 15

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

source

ORIGIN

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86650 CARATAGITCTICARATGGGGCCCCAGATGCAGTCCATGACTAAGATCCACGGGGCCC 36591
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Homo sapiens genomic DNA, chromosome 21q, section 18/105.
AP001674 AL163219 BA000005
AP001674.1 GI:7768666
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Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
Zimmernann,R., Roeenthal,A., Kudp,J., Shibuya,K., Kawasaki,K.,
Antonarakis,S., Shintani,A., Sasaki,K., Nagamine,K., Mitsuyama,S.,
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G.,
Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
Reichelt,J., Kauer,G., Blockker,H., Ramser,J., Beck,A., Klages,S.,
Hennig,S., Riesselmann,L., Dagand,E., Wehrmeyer,S., Borzym,K.,
                                                                                                                                                                                              CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  Length 174019;
                                                  Indels
  Score 556.6; DB 9;
Pred. No. 2.1e-164;
0; Mismatches 39;
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Query Match
Best Local Similarity 93.7%;
Matches 580; Conservative
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AUTHORS
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SOURCE
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     168885 AGGACTAGCTGGATTTCCTAGGCCAACTAAGAAGCCCTAAGCTAAGCTGGAAGATGACC 168826
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Homo sapiens genomic DNA, chromosome 21q21.1-q21.2 clone:B853K11,
LL56-APP region, complete sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                   169005 GABATCTCAACTGCCCAACCCCTACTATGCCCCCAATTCAGCAGGAAGCAGTTAGAGCCGT
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Published Only in DataBase (2000)
2 (Dases 1 to 174019)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
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S Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
Battori,M., Fujiyama,A., Ishli,K., Totoki,Y., Choi,D.K., Soeda,E.,
Ohki,M., Takadi,T., Sakaki,Y., Tatodien,S., Blechschmidt,K.,
Ohki,M., Takadi,T., Sakaki,Y., Tatodien,S., Blechschmidt,K.,
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Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Matsuyama,S.,
Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G.,
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Hennig,S., Riesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K.,
Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing
Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
Group * Institute of Molecular Biotechnology, Genome Analysis *
Keio University School of Medicine, Dept. of Molecular Biology *
GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics (addresses see below)
On May 30, 2000 this sequence version replaced gi:7717271.
The chromosome 21 mapping and sequencing consortium consisting of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
  Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
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* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
info.genome@gbf.de
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* Innestrasse 73, D-14195 Berlin, Germany,
* e.mail: info-chrzl@molgen.mpg.de
* MRL: http://chrzl.rz-berlin.mpg.de/
AL163219: Submitted (10-Apr-2000).
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Nature 405 (6784), 311-319 (2000)
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* e.mail: nshimizu@dmb-med.keio.ac.jp

* URL: http://www.dmb.med.keio.ac.jp/
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* e.mail: hattori@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
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27381 CAACCCCCTTTGGGTCCCCTGCCTTTGTATGGGAGCTCTGTTTTCACTCTATTCACTCT 27322
                                                                                                                                                                                                                                              Homo sapiens chromosome 18 clone RP11-762G24 map.18q21, WORKING DRAFT SEQUENCE, 13 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Physical
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bunamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 149755)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yadai,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 149,755 genomic DNA of 18q21
Published Only in DataBase (2000)
2 (bases 1 to 149755)
2 (bases 1 to 149755)
Published A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted Clares (24-MAR. 2000) Masahira Hattori, The Institute of Physicand Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (B-mail:hattoriège:riken.go.jp, URL:http://hgp.gec.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924) on Jul 14, 2000 this sequence version replaced gi:8117383.

Center: RIKEN Genomic Sciences Center (GSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Conter clone name: RP11-762024
Conter clone name: RP11-762024
Conter clone name: RP11-762024
Contencing vector: PCR products; 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 145596 bases at least Q40
Consensus quality: 1477102 bases at least Q30
Consensus quality: 1477102 bases at least Q30
Consensus quality: 1477102 bases at least Q30
Consensus quality: 14955; sum-of-contigs
Quality coverage: 10.98x in Q20 bases; sum-of-contigs
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HTG; WHCS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
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146768 148219 contig of 1452 bp in length
148320 149755 contig of 1436 bp in length.

* NOTE: This is a "working draft' sequence. It currently
consists of 13 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                          gap of 100 bp
contig of 18642 bp in length
gap of 100 bp
contig of 14761 bp in length
gap of 100 bp
gap of 100 bp
                                                                                                                                                                                                                                                                                             9: gap of 100 bp
6: contig of 3697 bp in length
5: gap of 100 bp
7: contig of 4024 bp in length
9: gap of 100 bp
1: contig of 2711 bp in length
1: gap of 100 bp
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of 6471 bp in length
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44929. .82602
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Length 149755;

Score 551.8; DB 2; Pred. No. 6.8e-163;

86.9%; 91.8%;

Query Match Best Local Similarity

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67367 Aggachagchgeartricchaggchgachaagarcchaaacchagchggaagargach 67426
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(Composition of 152980)

(Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Coolge, S., Paro, S., Perreitz, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lehoczky, J., Levine, R., Liu, G., Machean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,
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Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-762G24
Unpublished
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                                          TGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                     CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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Homo sapiens chromosome 18 clone RP11-762G24 map 18.
AC090313
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HTG; HTGS PHASB2; HTGS_FULLTOP; HTGS_CANCELLED.
Homo sapiens (human)
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VERSION
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(Bases 1 to 15298)

Barran, N. Bastien, V. Bloom, T. Boquelavky, L., Boukgalter, B.,

Cook, A., Cooke, P., Chararo, B., Choepel, Y., Collymore, A.,

Cook, A., Cooke, P., Fitzderald, M., Gage, D., Galgan, J.,

Faro, S., Ferreira, P., Fitzderald, M., Gage, D., Galgan, J.,

Gardyna, S., Gord, S., Graham, L., Johnson, R., Lindblad, Toh, K.,

Liu, G., MacLean, C., Landers, T., Levine, R., Lindblad-Toh, K.,

Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,

Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. Houndry, T., Naylor, J., Meneus, L., Mihova, T., Menga, V.,

Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,

Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,

Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Aug 6, 2002 this sequence version replaced gi:21699527.

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Scaman, S., Severy, P., Strauss, N., Stojanovic, N., Strauss, N., Stojanovic, N., Strauss, N., Travis, N., Trigilio, J., Vassiliev, R., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                      Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 152980: contig of 152980 bp in length.
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/clone="RP11-762G24"
/clone_lib="RPC1-11 Human Male BAC"
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91.8%; Pred. No. 6.8e-163;
ive 0; Mismatches 52;
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/db_xref="taxon:9606"
/chromosome="18"
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Center clone name: 762_G_24
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Best Local Similarity 91.8
Matches 583; Conservative
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Direct Submission
Submitted (31-AUG-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (16-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Nov 16, 2001 this sequence version replaced gi:15383820.
Draft Sequence Produced by DOE Joint Genome Institute
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Catarrhini, Hominidae, Homo.
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CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                       CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                                                           CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116928 ACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCCAATCATTGCCTG 116869
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                                                                                                                                                                                                                                                                                                                                                           117288 CAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAAAATCTACCGTGGACCC 117229
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGACTGAGAGAC
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                                                                                                                                                                                                                                                                                                                                    CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                             86.9%; Score 551.8; DB 9; Length 163803; 93.2%; Pred. No. 6.9e-163;
                                                                                                                                                                                                                                                                                                  ö
   www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
Finishing Completed at Stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                              1. .163803
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                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                   577; Conservative
                                                                                                                                                                                                                                                                                Similarity
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AC107075/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-MAY-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 176425)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entire insert of this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this colone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (15-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. M 63108, USA
4 (bases 1 to 176425)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (12-JUN-2002) Department of Genetics, Washington
University, 444 Forest Park Avenue, St. Louis, Missouri 63
On May 30, 2002 this sequence version replaced gi:18640713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                              2 (bases 1 to 176425)
Swearengen-Shahid, S., Meyer, R. and Dignan, G.
The sequence of Homo sapiens BAC clone RP11-452N17
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                 Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: H_NH0452N17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- Summary Statistics
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1 (bases 1 to 176425)
Sulston, J.E. and Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 176425)
Waterston, R.H.
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241 CATCAGCCAACTCCCCAACAGCACTTCGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 300
160828 CTTCGGCCAACCTCCCCAAAAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 160769
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Polymorphisms exist between AC110086 and AC107075. Data from AC110086, AC116626 and AC018872 was used to finish AC107075. Location/Qualifiers
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repeat_region	24825839 404	86.9%; Score 92.8%; Pred. vative 0; Mir	GTATCTTTAACCTCCTTGTTAAG		TTGTTCTTCAAATGGAGCACCAG	ACCGGCCTGCTAGCCCATGCTCC		TCTCAACTGCACACCCCTACTA
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301 AGGACTAGCTGGATTTCCTAGGCCAACGAATCCCTAAGCCTAGCTGGGAAGGTGACT 360

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                                                                                                                                                            chromosome="6'
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Submitted (05-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone request@sanger.ac.uk

On Nov 20, 2000 this sequence version replaced gi:11125403.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw.: SWISSRROT; Tr:, TREMBL; Wp:, WORWEEP; Information on the WORNEP database can be found at their source databases:

Em:, EMBL; Sw.: SWISSRROT; Tr:, TREMBL; Wp:, WORWEEP; Information chttp://www.sanger.ac.uk/Projects/Calegans/wormpep This sequence has generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr6

IMPORTANT: This sequence is not the entire insert of clone RPII-12BI3 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RPII-12BI3 is at 1 in this sequence. The true right end of clone RPII-12BI3 is at 1 in this sequence and alternate chemistry or covered by high quality data (i.e., phred quality >= 30) an attempt was made to resolve all sequenced by the group problems, such as compressions and repeats; all regions were either double-stranded or sequenced by the group problems, such as compressions and reseats; all regions were of the assembly was confirmed by restriction digest.

RPII-12BI3 is from the library RCI-11.1 constructed by the group of Pieter de Jong. Por further details see
                                                                                                                                                                                                                                                                                                                                                                                                           160528 CGGCAACAGCAACCCCCTTTGGGTCCCCTTTGTATGGGAGCTCTGTTTTCACTCTA 160469
                                                                                                         160708 GCTTCCATCTTTAAACACGGGCTTACAACTTAACTCACACATGACCAATCAGATAGTAA 160649
                                                                                                                                                                                                   160588 TGTTGCCTGAGAGCACAGCGGAGGGACAATGATCGGGATATAAACCCAGGCATTCAAGC 160529
AL139090 128468 bp DNA linear PRI 12-APR-2001 Human DNA sequence from clone RPI1-12B13 on chromosome 6 Contains STSs and GSSs, complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 128468)
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                                                                                                                                                                    413 -GAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
                                                                                                                                                                                                                                                                           472 TATTGCCTGAGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGC
                                                             GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCA-
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/Jobe="L2 repeat: matches 2574. .2704 of consensus"
2290. .2509
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..2509 ..2509
..2509 ..2509
..2509 ..2509
..2312
/note="L2 repeat: matches 1693. .2089 of consensus"
3497. .3568
/note="MER20 repeat: matches 16. .188 of consensus"
complement (4521. .5085)
/note="match: GSS: Em:AQ421033"
/note="match: GSS: Em:AQ483615"
complement (4633. .5083)
/note="match: GSS: Em:AQ883615"
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/note="LIMEc repeat: matches 1469. 1910 of consensus"

complement(18475. 18995)

/note="match: GSS: Em:AQ755181"

18938. 19072
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/nocte="LIME3 repeat: matches 4381. .6140 of consensus"
8806. .939
/note="LIPA5 repeat: matches 5526. .6143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="LIMEc repeat: matches 2408. .2260 of consensus"
[7741. .18039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="LIMEc repeat: matches 2106. .2409 of consensus"
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/note="MER41B repeat: matches 114. .601 of consengus"
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note="LTR16B repeat: matches 97. .464 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        consensus,
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/note="MERSA repeat: matches 3. .186 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSx repeat: matches 1. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6085. .6174
/note="MIR repeat: matches 64. .153 of consensus"
                                                                                                                                                                                                                   .966 of consensus"
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83289. .23682
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/note="AluJo repeat: matches 120.
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/note="match: GSS: Em:AQ544837"
clone lib="RPCI-11.1"
1. .353
note="match: GSS: Em:AQ609536"
                                                                                                           Em: AQ704228"
                                                                                                                                                                                             571. .1535
/note="LTR5 repeat: matches 1.
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RESULT 22
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43255. 43365
//note="LIM4 repeat: matches 2169. 2266 of consensus"
43366. 43774 repeat: matches 1. .426 of consensus"
//note="MSTA repeat: matches 2266. 2691 of consensus"
//note="LIM4 repeat: matches 6093. 6289 of consensus"
//note="LIMA7 repeat: matches 6093. 6289 of consensus"
//note="LIMB8 repeat: matches 5658. 6169 of consensus"
//note="LIMB8 repeat: matches 5658. 6169 of consensus"
                                                                                                  24638 ..2484 | American September 126 | Americ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13176. .33500
note="LTR17 repeat: matches 1, .326 of consensus"
13501. .33791
note="HERV17 repeat: matches 8244. .8523 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13811. .38137

//note="HERV17 repeat: matches 1651. .5933 of consensus"

18135. .39557

//note="HERV17 repeat: matches 1. .1836 of consensus"

18958. .40489

//note="LTR17 repeat: matches 257. .780 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10490. .41321

// Anote="LiME3A repeat: matches 5261. .6131 of consensus"

11354. .41655

11971. .42279
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Complement (50811. 51360)

Anote="match: GSS: Em:AQ536659"

Anote="LiPA3 repeat: matches 2255. .6146 of consensus"
56710. .57178

Anote="MIRTIC repeat: matches 1. .463 of consensus"
Anote="MIRTIC repeat: matches 202. .323 of consensus"
F7746. .57869

Anote="MIRTIS repeat: matches 202. .323 of consensus"
57746. .57869

F7869. .58554
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/note="LiM4 repeat: matches 4637. 4856 of consensus" 47481. 47839
47481. 48031
/note="Will4 repeat: matches 8. 345 of consensus" 47848. 48031
/note="Will4 repeat: matches 4451. 4645 of consensus" 48017. 49417
/note="LiM4 repeat: matches 2373. 3522 of consensus" 49436. 50712
                                                                                                                                                                                                                                                                                                                                                                                                                                                        73298. .32650
/note="1.1M4 repeat: matches 4626. .4909 of consensus"
32799. .32963
32799. .32963
33151. .33174 repeat: matches -2. .162 of consensus"
/note="12 copies 2 mer tt 95% conserved"
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/note="AluSq repeat: matches 1. .307 of consensus"
59630. .60070
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/note="MER33 repeat: matches 1. .202 of consensus"
                             'note="MIR repeat: matches 90. .141 of consensus"
                                                        24395, .24791
/note="match: GSS: Em:AQ027280
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33372 ACTAAGAAGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCAATTGCCTG 33313
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Human DNA sequence from clone RP11-456B18 on chromosome 13,
complete sequence.
AL139038 AL139038.18 GI:14800148
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                              CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (14-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
    repeat: matches 5737. .6184 of consensus
                                                                                       consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
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                                                                                                                                                                                         Gaps
                                                                                                                                              Length 128468;
                                                                                                                                                                                      3;
                                                                                     .6164 of
                                                                                                                                                                                      Indels
/note="L1MB3 repeat: matches 5737.
59956. .60646
/note="match: GSS: Em:BB2923"
61550. .61582
/note="1,1ME2 repeat: matches 6133.
61583. .62103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.8%; Score 551.4; DB 9; Best Local Similarity 93.9%; Pred. No. 8.9e-163; Matches 596; Conservative 0; Mismatches 36;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 140756)
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Dunn, M.

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29729. .29752
/note="12 copies 2 mer tg 95% conserved"
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                               .151
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                             repeat: matches 2.
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requests: clonerequest@sanger.ac.uk
On Jul 17, 2001 this sequence version replaced gi:13751261.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the voratation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WORMPEP; Information on the WORMPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ductuaise can be round a cut, Projects/C elegans/wormpep This sequence buttp://www sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.aanger.ac.uk/HGP/Chr13
RP11-456B18 is from the library RPC1-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
NPCTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP1-456B18 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true right end of clone RP11-456B18 is at 140756 in this sequence. The true left end of clone RP11-78116 is at 68441 in this sequence. The true right end of clone RP11-108H9 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .6146 of consensus"
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note="MER4D repeat: matches 483. .677 of consensus"
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note="LTR29 repeat: matches 6. .203 of consensus"
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/note="MLT2D repeat: matches 1. 486 of consensus"
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Celone="RP11-456B18"
Celone="1216"
1830. -2326
note="LORIa repeat: matches 1. .497 of consensus"
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/note="LOR1b repeat: matches 1. .461 of consensus"
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note="LTR8 repeat: matches 1. .691 of consensus"
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note="L1ME3 repeat: matches 6002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="HERV23 repeat: matches 993.
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note="LTR16A repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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'note="17 co
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note="MSTC-internal repeat: matches 2. .1651 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anote="Limb2 repeat: matches 5277. .5594 of consensus" 21308. .21570 // note="Limb3 repeat: matches 357. .625 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 5400. .6155 of consensus"
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23498. .23784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1MC4 repeat: matches 6409. .6540 of consensus"
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11648. .31785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MER66A repeat: matches 1. .69 of consensus"
6570. .16629
'note="MER41B repeat: matches 283. .341 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MER54B repeat: matches 585. .789 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MER54B repeat: matches 112. .278 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MER66A repeat: matches 163. .478 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="LIP repeat: matches 1726. .2897 of consensus" 9460. .19584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .393 of consensus"
'note="MER67D repeat: matches 12. .391 of consensus"
                                                                                                                                                                                        'note="MER4D repeat: matches 396. .973 of consensus"
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25044. .25238
                                                                                                                                                                                                                 /note="THE1B repeat: matches 1. .364 of consensus"
13222. .14798
                                  11249. 11332
1.00ce="WIR repeat: matches 69. .144 of consensus"
1723. 12159
17note="WER4D repeat: matches 1. .234 of consensus"
                                                                                                                                                                                                                                                                                                                                                                         14799. .15173
/note="THE1B repeat: matches 1. .364 of consensus"
16144. .16346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .305 of consensus"
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                                                                                                                                                                                                                                                                                                          'note="THE1B-INTERNAL repeat: matches 1. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluY repeat: matches 1. .297 of consensus" [8120. .1929]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="15 copies 5 mer atttt 62% conserved" 19686. 19745
'note="12 copies 5 mer tttaa 71% conserved"
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ACTABABATGCTBACTBGGCBABABCBGGBGGTBABGBABTBGCCBATCATCTBTTGCCTG 69656
                                                                                                                                 69657 AAAGCACAGCGGGAGGGACAAGGATCGGGATATGAACCCAGACATTCGAGCCGGCAACAG 69716
                                                                                                                                                                                                                                                                                                                                             AC021774 167366 bp DNA linear HTG 30-MAR-2000
Homo sapiens clone RP11-13C19, WORKING DRAFT SEQUENCE, 10 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                         AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
Center clone name: 13_C_18
Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 161819 bases at least Q40
Consensus quality: 164760 bases at least Q30
Consensus quality: 165688 bases at least Q30
Insert size: 170000; agarose-fp
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------ Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 167366)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-13C18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluJo/FRAM repeat: matches 197. .297 of consensus"
                                                                                                                                               /note="MERGY repeat: matches 202. .403 of consensus" 3979. .3868
//note="Liphiz repeat: matches 6076. .6152 of consensus" 40953. .41258
//note="AluY repeat: matches 1. .308 of consensus" 41279. .41308
//note="Lip copies 2 mer aa 86% conserved" 42744. .42933
//note="Lib copies 2 mer aa 66% conserved" 42744. .42933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49853. .50271
/note="LIMBc repeat: matches 2274. .2369 of consensus"
60637. .50927
/note="LIME repeat: matches 974. .1253 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45800. .45851
/note="MLT2B repeat: matches 394. .448 of consensus"
48118. .48487
/note="THELC repeat: matches 1. .370 of consensus"
48708. .48806
                                                                                                                                                                                                                                                                                                                         42973. .43275
/note="AluSx repeat: matches 1. .303 of consensus"
complement(43560. .43991)
/note="match: STS: Em:HSPH07E5"
45196. .45584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 131. .228 of consensus" 52696. .52996 /note="AluSg repeat: matches 1. .293 of consensus"
                                                                                                                 .360 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                           .399 of consensus"
                       consensus
                                                       /note="THE1C-internal repeat: matches 3. .1651 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 551.4; DB 9; Length 140756;
Pred. No. 9e-163;
0; Mismatches 31; Indels 4; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="87 copies 2 mer ta 77% conserved"
                     φ
                     .371
                   'note="THEIC repeat: matches 1.
                                                                                           34465. .34825
/note="THELC repeat: matches 1.
34804. .35004
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MLT2B repeat: matches 2.
45594. .45767
                                       32824. .34464
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Best Local Similarity 94.3%;
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 167366;
              Insert size: 166466; sum-of-contigs
Quality coverage: 4.8 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                      1372: contig of 1272 bp in length
1372: gap of 100 bp
4088: contig of 2716 bp in length
4188: gap of 100 bp
6500: contig of 2312 bp in length
6600: gap of 100 bp
15485: contig of 8885 bp in length
15585: gap of 100 bp
27677: contig of 12052 bp in length
27677: gap of 100 bp
277377: gap of 100 bp
277377: gap of 100 bp
87781: gap of 100 bp
54618: contig of 14560 bp in length
68725: contig of 28007 bp in length
82825: gap of 100 bp
123332: contig of 4407 bp in length
123332: contig of 4407 bp in length
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/db_xref="taxon:9606"
/clone="RP11-13C18"
/clone lib="RPCI-11 Human Male BAC"
1. 1.72
/note="assembly_fragment"
1373. 4088
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llarity 93.9%; Pred. No. 9.3e-163;
Conservative 0; Mismatches 36;
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6601. 15485
/note="assembly_fragment"
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/note="assembly_fragment"
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61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120

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HTG; HTGS_PHASE2; HTGS_CANCELLED.
HTG; HTGS_PHASE2; HTGS_CANCELLED.
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission

Submitted (18-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Oct 5, 2001 this sequence version replaced gi:15962724.
                                                                                                                                                                     481 AGAGCACAGCGGGGGGGACAAGGATCGGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                       GAAATCTCAACTGCACAAACCCCTACTATGACCCAATTCAGCAGGAAGCAGTTAGAGCAGT
                                                                                                                                               CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGACTGAGAGA
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CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                       GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
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AL607153
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AP002790 164211 bp DNA linear HTG 13-JUL-2000 Homo sapiens chromosome 18 clone RP11-732P12 map 18q21, WORKING DRAFT SEQUENCE, 20 unordered pieces.
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                                                                                                                                                                                                                                                                                            Bukaryogia, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases I to 164211)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T. Totoki,Y., Watenabe,H. and Sakaki,Y. Published Only in DataBase (2000)
2 (bases I to 164211)
2 (bases I to 164211)
2 (bases I to 164211)
2 Lattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watenabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUL-2000) Masahira Hattori, The Institute of Physicand Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(B-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: 5.05x in Q20 bases; sum-of-contigs
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Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
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HTG; HTGS PHASE1; HTGS_DRAFT.
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                                                                                            * NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 183499: contig of 183499 bp in length.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Insert size: 179011; 5.6% error; agarose-fp
Quality coverage: 12.84x in Q20 bases; sum-of-contigs Quality
coverage: 13.23x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.8%; Score 551.4; DB 2; Length 183499; Best Local Similarity 94.3%; Pred. No. 9.4e-163; Matches 584; Conservative 0; Mismatches 31; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="13"
/clone="RP13-276D12"
/clone lib="RPCI-13.2"
1. .183499
/note="assembly_fragment:05362"
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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Physical

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CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
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                 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTCAGAGGGGGTACTGAGAGAC
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Pred. No. 2.2e-162;
0; Mismatches 53;
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16024. .162721
/note="assembly_fragment"
16382. .164211
/note="assembly_fragment"
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58433. .160143
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150443. .153002
'note="assembly_fragment"
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155325. .156567
                                                                                                                                     47744. .150342
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Best Local Similarity 91.7%;
Matches 582; Conservative
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NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                 contig of 28606 bp in length
gap of 100 bp
contig of 27267 bp in length
gap of 100 bp
contig of 17628 bp in length
gap of 100 bp
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gap of 100 bp
gap of 100 bp
                                                                                                                                                                                                                                                                                                              3: gap of 100 bp
1: contig of 9558 bp in length
1: gap of 100 bp
1: contig of 8982 bp in length
3: gap of 100 bp
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5: contig of 4379 bp in length
5: gap of 100 bp
5: contig of 4419 bp in length
7: gap of 100 bp
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158432: contrig of 1665 bp in length
158432: gap of 100 bp
160143: contrig of 1711 bp in length
160243: gap of 100 bp
16221: contrig of 2478 bp in length
162821: gap of 100 bp
164211: contrig of 1390 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                  gap of 100 bp
contig of 8814 bp in length
gap of 100 bp
contig of 7370 bp in length
gap of 100 bp
contig of 6530 bp in length
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gap of 100 br
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/note="assembly_fragment"
10272. .111253.
/note="assembly_fragment"
111354. .120167.
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127738. .134267
/note="assembly_fragment"
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120268. .127637
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/note="assembly_fragment"
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/note="assembly_fragment"
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/organism="Homo sapiens'
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/db_xref="taxon:9606"
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Estrem, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, A., Cook, P., DeArellano, K., Cheepel, Y., Collymore, A., Gook, P., DeArellano, K., Daaz, J.S., Dodge, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Lindblad-Toh, K., Lindblad-Toh, K., Lindblad-Toh, K., Liudblad-Toh, K., Liudg, MacLean, C., Macdonald, P., Major, J., Matthews, C., MacCarthy, M., Meldrim, J., Meneus, L., Micol, R., Norbu, C., Norman, C., Murphy, T., Naylor, J., Ngrop, C., Nicol, R., Norbu, C., Norman, C., Phunkhang, P., Pleire, N., Raymon, C., Norl, D., Oliver, J., Peterson, K., Schauer, S., Schauer, A., Waynan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.
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                                                       ACO64801 167843 bp DNA linear PRI 30-JUL-2002
Homo saplens chromosome 18, clone RP11-120K19, complete sequence.
ACO64801
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 18, clone RP11-120K19
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Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Ries, C., Rogov, P., Roman, J., Roy, A., Schuer, S., Schupback, R., Seman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfave, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                        Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Ull 30, 2002 this sequence version replaced gi:21700673. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                            Contact: sequence submissions@genome.wi.mit.edu
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/clone lib=RFCI-II Human Male BAC"
complement (1059. 1111)
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complement (1112. 1424)
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1646. 1651
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1689. 1693
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8560. 8867
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8962. 9273
/rpt_family="AluSq"
11717. 11744
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complement(5559, .5607)
/rpt_family="A
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6353. .6769
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complement(2489. .2622)
/rpt_family="FLAM_C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic_DNA"
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4384, 4633
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'rpt_family="LTR16C"
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6770. .6846
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12041. .12266
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Human chromosome 14 DNA sequence BAC R-30513 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
AL121784
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1 (bases 1 to 180523)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottler,P., Cattolico,L., Barbe,V., Pelletier,B., Artiguenave,F., Gyapay,G., Saurin,W. and Weissenbach,J.
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Direct Submission

Submitted (01-AUG-2001) Genoscope - Centre National de Sequencage : Submitted (01-AUG-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

On Aug 23, 2001 this sequence version replaced gi:12001714.
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                                                                                                                                                                                           361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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Contact: SeqRef@genoscope.cns.fr
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llarity 91.7%; Pred. No. 2.2e-162;
Conservative 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                   /rpt family="AluJo"
complement (21102. .21388)
/rpt family="AluJb"
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complement(28729. .28847)
/rpt_family="LIMC/D"
29217. .29290
/rpt_family="L2"
                               /rpt_family="MRR50"
complement(14240..14530)
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1488I..1528R
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ement (1700
                                                                                                                                                                                                                                                                    complement (17998. 18430)
/rpt_family="MER65A"
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complement(29806. .30079)
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                                                                                                                                                /rpt_family="indictions" (somplement (15654 ... 15794) /rpt_family="MERSA"
                                                                                                                                                                                                                /rpt family="MLT2A2"
complement(17190..17503)
/rpt family="AluSx"
complement(17524..17861)
                                                                                                                rpt family="LTR16A1"
5290. .15645
rpt family="THE1C"
                                                                                                                                                                                                                                                                                                                                        /rpt_family="AT_rich"
complement(19903. .20
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21986. .22149
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2201. .22391
rpt_family="LTR67"
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family="MLT1C"
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|2512. .13031
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PRI 27-MAR-2001

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Classes I to 190565)

Rowen, L., Madan, A., Qin, S., Abbasi, N., Dors, M., Dickhoff, R.,
James, R., Loretz, C., Lasky, S., Madan, A., Prescott, S., Ratcliffe, A.,
Shaffer, T. and Hood, L.
Direct Submission

Submitted (25-APR-1999) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
3 (bases I to 190565)

Surke, J., Dors, M., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,
Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,
Pate, D. and Hood, L.
                                                                                               957 ACTAAAATGCTAATTAGGCAAAAACAGGGAAAGGAAATAGCCAATCATCGCCTG 1016
                                                                                                                                                                       541 CAACCCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT 600
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Submitted (27-MAR-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. (base) 1 to 19055)
Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,
                                                                                                                                                                                                                                                                                                                                                          AC007374 190565 bp DNA linear PRI 27-MAR-20
Homo sapiens chromosome 14 clone RP11-325L17 map 14q31, complete
                                                                           481 AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98105, USA
On Mar 27, 2001 this sequence version replaced gi:8247780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pate, D. and Hood, L. Sequencing of human chromosome 15 D15S146-D15S117 region Unpublished
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Center code: UMNSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen@systemsbiology.org
Contact: leerowen@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP11-325L17"
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985. .1035
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Homo sapiens (human)
Homo sapiens
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7100e="matching EMBL:AA010373

RHdb:RHSSSTSSST

dbSTS:STSSSST0

Identified using the e-PCR software (G. Schuler)"
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Location/Qualifiers
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92.9%; Pred. No. 5.4e-162;
iive 0; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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/clone lib="RPCI-11"
1561. .1825
                                                                                                                                                                                                                                                                                                                                                                            chromosome="14"
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Overall quality chart
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Human chromosome 14 DNA sequence BAC C-2547L24 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (04-MAY-2001) Genoscope · Centre National de Sequencage :
BP 191 91006 EVRY cedex · FRANCE (E-mail ; segref@genoscope.cns.fr
                                                                                                                                                                    009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 20377) Hellig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiquenave, F., Gyapay, G., Saurin, W. and Weissenbach, J. Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end) : R-305I3
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                                                                                                                                                                 541 CAACCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Web : www.genoscope.cns.fr)
On Jun 3, 2000 this sequence version replaced gi:7406569.
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1. 203777 /organism="Homo saplens"
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                                                                                                                                                                                                                                                                                                                 23607 ATTAAATCTTGCAACTGCAAAAACAAAACAAAA 23641
                                                                                                                                                                                                                                                                                 601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAA 635
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2 (bases 1 to 203777)
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117677. 117680
/note="low quality data"
117730. 117748
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Pred. No. 5.5e-162;
0; Mismatches 35; Indels 10;
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Anote="10w quality data"

46695. 46700

/note="10w quality data"

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110860. 110875
                                  1865. .3870
"note="low quality data"
1875. .14880
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113613. .113617
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16230. .116782
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144847. .144850
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[52067, .15207]
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177622. .177705
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/note="low quality data"
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.7488. .17535
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118505. .118736
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherta; Primatee; Catarrhini; Hominidae; Homo.

(bases 1 to 11254)

Mammalia; Eutherta; Primatee; Catarrhini; Hominidae; Homo.

(bases 1 to 11254)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Albertaid,J., Banks,T., Barbarta,J., Banks,T., Barbarta,J., Banks,T., Barbarta,J., Banks,T., Barbarta,J., Banks,T., Barbarta,J., Bonnin,D., Bands,C., Bonch,D., Brown,M., Barks,T., Barbarta,J., Barbarta,J., Barketh,C., Burch,P., Burketh,C., Burch,J., Charles Collon,C., Coyle,M., Carcon, C., Coyle,M., Dadhand,C., Coyle,M., Dadhand,C., Danys,C., Coyle,M., Dadhand,C., Danys,C., Dayy-Carroll,L., Dederich,D., A., Dalaney, K.R., Delgac,O., Denn, A.L., Ding,Y., Dith, H., Delaney, K.R., Drager,D., Edward,C.C., Elhaj,C., Escotto,M., Falls, M., Gavaza,M., Gunarathe,P., Hale,S., Hamilton,K., Harriandez,O., Harriag,K., Hart,M., Hards,M., Garrell,J., H., Guevaz,M., Gunarathe,P., Hale,S., Hamilton,K., Harriandez,O., Harriag,K., Hart,M., Haves,M., Holloway,C., Harriag,K., Hart,M., Hards,M., Hawes,M., Holloway,C., Kratovic,J., Howad,S., Kah, M., Hawes,M., Holloway,C., Kratovic,J., Mohabat,M., Lidu,J., Li,J., Li,J., Lidu,J., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Martin,R., Mansey,R., Manneshwari,M., Moorish,T., Morte,J., Peters,J., Peters,J., Peters,J., Peters,J., Peters,J., Polychon, J., Peters,J., Peters,J., Peters,J., Polychon,R., Soberer, C., Spack,A., Standy,H., Stone,H., Suteon,B., Soberer, C., Spack,R., Stand,H., Shooshtari,M., Nayuen,N., Nayuen,M., Soberer, Sonaise,T., Spacks,A., Stands,M., Tomas,S., Ward,Moore,S., Workerson,B., Nayuen,S., Nayuen,H., Stone,H., Suteon,J., Peters,J., Peters,J., Peters,J., Polychokan,J., Roben,B., Stanery,G., Savery,G., Scott,G., Shan, Stanery,G., Stanery,G., Walliamson,A., Tameriaa,A., Tameriaa,A., Tang,H., Stone,J., Sonaise,T., Spacks,A., Stanley,R., Wall,M., Wall
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                                                                        9913 ACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATCGCCTG 9854
                                                                                                                                                                                  9793 CTACCCTCTTTGGGTCCCCTCCCTTTGTATGGGAGCTCAGT------TTTCACTCT 9744
                                                 AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                        541 CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
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Unpublished
2 (bases 1 to 112544)
Worley, K.C.
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Homo sapiens
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Identified using the e-PCR software (G. Schuler)"
42379. .42560
//note="matching EMBL:N80119
                                                                                                                                                                                                                                                                                                                                                                                                                               Identified using the e-PCR software (G. Schuler)"
145247. .145418
/note="matching EMBL:T02957
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Identified using the e-PCR software (G. Schuler)"
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Identified using the e-PCR software (G. Schuler)"
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Pred. No. 5.5e-162;
0; Mismatches 35; Indels 10;
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/clone_lib="CalTech-D"
9045. .9309
/note="matching EMBL:R74544
RHdb:RH53560
                                                                                                                                                                                                                     16628. .16834
/note="matching EMBL:G20331
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dbSTS:STS39514
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Best Local Similarity 92.9%;
Matches 590; Conservative
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Length 112544;
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complement(20156. 20458)
/rpt_family="Alusg1"
complement(20459. 20559)
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complement (2834. .3134)
/rpt_family="Aluy"
complement (3135. .3392)
/rpt_family="LiM4"
5391. 5415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MER5A"
22051. .22000
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(5454. .15878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="AT_rich"
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complement (7505. .7618)
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/761 .8048
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16207. 16227
/rpt_family="AT_rich"
16946. 17002
              /rpt_family="AluJ/FLAM"
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2313. .12350
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173. .7203
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[8059. .18361
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21217. .21344
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4236. .14529
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1176. .11213
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complement(15115.
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20687. .20790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GISS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
  Direct Submission
Submitted (09-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 112544)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (15-00T-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 26, 2002 This sequence version replaced gi:20976483.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                          Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 112544)
                                                                                                                                                                                                                                                                                            Submitted (26-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 112544)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (46. 1498)
/rpt family="LiM4"
complement (1499. 1804)
/rpt family="AluGa"
complement (1805. 2516)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                         Direct Submission
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Macciles 567; Collservacive U; Mis	minimaccines 4/; inders 1; daps	1
1 CCCTGTATCTTTAACCTCCTTGTTAA	CTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA	09
34048 CCCTGTATCTTTAACCTCCTTGTTAA	CCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCGAAGCTGTAAAACTA	34107
61 CAAATTGTTCTTCAAATGGAGCACCA	CAPATIGITCITCAPATGGAGCACCAGGAGGGGTCCATGACTAAGATCCACGGGACCC	120
34108 CAAATCGTTCTTCAAATGGAGCCCCC	CAAATCGTTCTTCAAATGGAGCCCCCAGATGCAGTCCATGACTAAGATCTACCGCGGACCC	34167
121 CTGGACCGGCCTGCTAGCCCATGCTC	TIGGACCGGCCTGCTAGCCCATGCTCCGGATGTTAATGACATTGAAGGCACCCCTCCCGAG	180
34168 CTGGACCGGCCTGTTAGCCCATGCGC	CTGGACCGGCCTGTTAGCCCCATGCGCTGATAATGACATCAAAGGCACCCCTCCCGAG	34227
181 GAAATCTCAACTGCACAACCCCTACT	CTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT	240
34228 GAAATCTCAACTGCACCACCCCTACT	GAAATCTCAACTGCACCACCCCTACTACGTGCCAATTCAGCAGGAAGCAGTTAGAGCAGT	34287
241 CATCAGCCAACCTCCCCAACAGCACT	CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGC	300
34288 CATCGGCCAACCTCCCCAACAGCACT	CATCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGCTGAGAGTGGGGACTGAGAGAC	34347
301 AGGACTAGCTGGATTTCCTAGGCCAA	AGGACTAGCTGGATTTCCTAGGCCAACGAATCCCTAAGCCTAGCTGGGAAGGTGACT	360
34348 AGGACTACCTATTCCTAGGCCG	AGGACTAGCTACATTTCCTAGGCCGACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACC	34407
361 GCATCCACCTCTAAACATGGGGCTTG	GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC	420
34408 GCATCCACCTTTAAACACGGGGCTTG	GCATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTGATCAATCA	34467
421 ACTAAAATGCTAATTAGGCAAAAATA	ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG	480
34468 ACTAAAATGCTAATTAGGC-AAAACA	ACTAAAATGCTAATTAGGC-AAAACAGGAGGTAAAGAAATAGCCAATCATCTACTGCCTG	34526
481 AGAGCACAGCGGGAGGACAAGGATC	AGAGCACAGGGGAGGGACAAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG	540
34527 ACAGCACAGTGGGAGGGACAAGGATC	ACAGCACAGTGGGAGGGACAAGGATGGGGATGTAAACCCACGCATTCAAGCCGGGAACAG	34586
541 CAACCCCTTTGGGTCCCCTCCCTTGTATGGCCGCTCTGTTTTCA	TGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT	009
34587 CAACCCCTTCGGGTCCCCTCTTT	CAACCCCCTTCGGGTCCCCTCTTTGTATGGGAGCTCTGTTTTCACTCTATGTCACTCT	34646
601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAAAAAAAA	AAAAAAAAA 635	
34647 ATTAAATCTTGCAACTGCAAAAAAAAAAAAAAAAAA		

Search completed: January 22, 2005, 16:13:43 Job time : 2674.68 secs

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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1. geneseqn1980s:*

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7. geneseqn2003ss:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

70	Description	Aav43215 Multiple	Aax29702 Clone CL6	Adg14843 MSRV asso	Adb84397 MSRV-1 as	Aaa63826 Nucleotid	Aad41225 Human EMB	Aav43219 Multiple	Aax29704 Clone 5M6	Adg14849 MSRV asso	Acc46747 Human dit	Adb84403 MSRV-1 as	Aax77526 Human sec	Aaz59468 Human sec	Adc38776 Human cDN	Abk89296 Human gen	Adq94981 Human kin	Aaf55630 Nucleotid	Aax25660 Human end	Aaa59210 3' pol ge	Aax25661 Human end	Aaa59211 5' non co
SUMMARIES	ΙD	AAV43215	AAX29702	ADG14843	ADB84397	AAA63826	AAD41225	AAV43219	AAX29704	ADG14849	ACC46747	ADB84403	AAX77526	AAZ59468	ADC38776	ABK89296	AD094981	AAF55630	AAX25660	AAA59210	AAX25661	AAA59211
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	Query Match Length DB	635	635	635	635	2030	2074	1329	1329	1329	2046	1329	2946	2946	2946	326014	326014	2781	1136	1136	2782	2782
d	Query Match	100.0	100.0	100.0	98.6	97.2	86.0	85.8	85.8	85.8	85.1	84.3	84.1	84.1	84.1	83.9	83.9	83.8	82.8	82.8	82.3	82.3
	Score	635	635	635	626	617.4	546.4	545	545	545	540.2	535	533.8	533.8	533.8	532.8	532.8	532.2	525.8	525.8	522.6	522.6
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44 Aah20069 HERV-W en Aad24195 Human syn Aad24195 Human syn Aaz25665 Complete Aax25665 Complete Aaa59215 Human ret Abn97978 Human ret Abn97929 Human ret Abn97929 Human ret Abn97929 Human ret Abn97929 Human foe Aai14608 Probe #44 Abn97929 Human foe Aai1880 Aba26337 Human bro Aba26337 Human bro Aba26978 Probe #44 Aba26978 Probe #44 Aba26978 Human bro Aba2663 Human Broben Aax2663 Human Gen Aba29213 Paxtial DAB064589 Human Gen Aax2663 Human end Aba29213 Paxtial DAB06892 Human rec Ada02882 Human rec Ada02882 Human PAP Ada02882 Human Car Ada02882 Human Car Ada02831 Mouse Pap Adm74477 Human car Ammans	irus fragment 4. irus; MSRV; MS; pol gene; gag gene; iated virus; 88.	protein AAW71067" ranhos-Baccala G; c. Mandfand B; - useful for diagnosis, prevention and sis. sh. multiple sclerosis (MS) associated used in the method of the invention. partial genomic sequences of the MSRV-
AAH20069 AAD24195 ABL6174 AAX25665 AAN592165 AAN97978	BP. retrov retrov s-assoc retrov ifiers	
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This sequence represents clone CL6-3' from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
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100.0%; Pred. No. 9.1e-187;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      Claim 1; Page 36-37; 83pp; French
                                                                                                         97FR-00008816,
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Best Local Similarity 100.
Matches 635; Conservative
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l pol gene, gag gene and env gene, and polypeptides encoded by these genes. The invention also provides antibodies raised against the polypeptides. The genomic sequences, polypeptides and antibodies are also claimed useful for diagnosing infection by MS and rheumatoid arthritisassociated viruses, and also for prevention and treatment of infection
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                                                                                                                             Seguence 635 BP; 188 A; 170 C; 136 G; 141 T; 0 U; 0 Other;
                                                                                                                                                              100.0%; Score 635; DB 2; Length 6
Larity 100.0%; Pred. No. 9.1e-187;
Conservative 0; Mismatches 0; Indels
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                                                                                          with these viruses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₩,
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                                                        AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGGTGGGAAGGTGACT
                                                                                                                                                                  GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGCTC
                                                                                                                                                                                                                                     ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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                             AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                    GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGCTC
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Jolivet-Reynaud C, Mandrand
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KOMURIAN-PRADEL F
JOLIVET-REYNAUD C
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BESEME F.
BEDIN F.
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GARSON J A
TUKE P W.
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(GARS/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid and their fragments having the pol gene of a retrovirus, useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid which comprises the gene of a retrovirus associated with multiple sclerosis or rheumatoid arthritis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis. The present sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuke
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                                                                                                                                                                                                                                                                                                                                                                                          multiple sclerosis; rheumatoid arthritis.
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pol, gag or reverse transcriptase genes (or their fragments) encoding the proteins or defined peptides (including immunodominant peptides.)

C antigenia peptides or conserved motifs) Also included are a process for detecting a virus associated with multiple sclerosis or rheumatoid arthritis, a prime for the amplification by polymerisation of a nucleic acid of a viral material associated with multiple sclerosis or rheumatoid arthritis, a primer for the amplification by polymerisation of a nucleic acid of a viral material associated with multiple sclerosis or rheumatoid or viral material associated with multiple sclerosis or rheumatoid or arthritis, a polypeptide exhibiting an inhibitory activity on the protecolytic, reverse transcriptase or ribonuclease H activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by communogenic agent consisting of the antigenic polypeptide defined above. The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis. The present sequence is a claimed MSRV-associated sequence whose identity cannot be accurately determined. Note: The SEQ ID numbers for the sequences as displayed in the main body of the patent do not match the SEQ ID numbers of the present of the sequence of the sequence of the consequently those sequences manifoled in the main body or consequently those sequences manifoled in the main body or the patent do not match the SEQ ID numbers of the present of the sequence of the seq
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Sequence 635 BP; 188 A; 167 C; 133 G; 138 T; 0 U; 9 Other;

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Score 626; DB 9; L
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The present sequence represents the nucleotide sequence corresponding to the 3' env region and long terminal repeat sequences from clone CL6 of Multiple Sclerosis retrovirus (MSRv-1). The specification describes a long terminal repeat (LTR)-RUS region which encodes the expression of MSRv-1 protein. This is unusual for LTRs, in particular in the RUS region. The sequence includes CAAT and TATA signals which are present in the U3 and R regions and are not directed towards the CDS indicated in the features table. Probes and antibodies to the MSRV-1 retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein and encoding polynucleotide sequences are used to detect the presence of MSRV-1 retrovirus in a biological sample. (Updated on 06-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide fragment of LTR-RU5 region from Multiple Sclerosis retrovirus (MSRV) used to detect the presence of MSRV-1 retrovirus in a biological
                                                                                                                    region; long terminal repeat; LTR; RUS region; retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2030 BP; 574 A; 559 C; 387 G; 510 T; 0 U; 0 Other;
                                                                                          Nucleotide sequence of the MSRV-1 3' env and LTR regions.
                                                                                                                                                                                                                   /*tag= a
/note= "Contains one termination codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Komurian-Pradel
                                                                                                                                                              Multiple sclerosis associated retrovirus.
                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 23pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99EP-00420041
                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-FEB-2000; 2000WO-IB000159
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1800. 1807
/*tag= c
1858. 1864
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                                                                  (first entry)
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1906.
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1996. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-506097/45.
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                                                                                                                                                                                                                                                                                                                                                          polyA_signal
                                                     06-AUG-2003
04-DEC-2000
                                                                                                                        MSRV-1; pol
                                                                                                                                                                                                                                               sig_peptide
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                                                                                                                                                                                                                                                                         CAAT_signal
                                                                                                                                                                                                                                                                                                    CAAT_signal
                                                                                                                                                                                                                                                                                                                               rATA_signal
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Indels

Score 617.4; DB 3; Pred. No. 4.8e-181; 0; Mismatches 11;

Query Match 97.2%; Best Local Similarity 98.3%; Matches 624; Conservative

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Length 2030;

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useful for screening modulators useful for treating or preventing useful for screening modulators useful for treating or preventing disorders associated with abnormal expression of EMBRY. The disorders treated include reproductive disorders such as infertility, endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory disorder such as acquired immune deficiency syndrome (AIDS), allergies, contact dermatitis; disorders of the placenta such as preeclampsia, abruptic placentae etc. Sequences of the invention are also useful for analysing a proteome of a tissue or a cell type. EMBRY proteins are useful as immunogens for preparing antibodies. Polynucleotides of the invention are useful for creating knockin humanised animals or transgenic animals to model human diseases. They are also used in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .759 AGGACTAGCTGGATTTCCTAGGCCGATTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACC 1818
                                                                                                                                                                                                                                                                                            New polypeptides of human embryogenesis associated proteins for screening modulators useful for treating or preventing disorders e.g. endometriosis, infertility, allergy, preeclampsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGGGACTGAGAGAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to human embryogenesis associated proteins (EMBRY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1519 CAPATGGTTCTTCAAATGGAGCCCCAGATGCAGTCCATGACTAAAATCTACCACGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1579 CTGGACCGGCCTGCTAGCCCCATGCTCGATGTTAATGACATCGAAGGCACTCCTCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1459 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATTGAAGCTGTAAAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 546.4; DB 6;
Pred. No. 5.9e-159;
0; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is human EMBRY-2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                       Claim 59; Page 96-97; 97pp; English.
                                          14-NOV-2001; 2001WO-US043956
                                                                                       15-NOV-2000; 2000US-0249407P
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93.8%;
                                                                                                                                  (INCY-) INCYTE GENOMICS INC.
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Best Local Similarity 93.8
Matches 579; Conservative
                                                                                                                                                                                                                          WPI; 2002-537629/57.
P-PSDB; AAE25054.
20-JUN-2002
                                                                                                                                                                               Ramkumar J,
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                                                                    CAGATGGTCTTACAAATGGAACCCCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                                          CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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                                                                                                                                    CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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                                             CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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*tag= b
14. .1689
*tag= c
/product= "Mature EMBRY-2 protein"
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/product= "EMBRY-2 protein'
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                                                                             257 cccrerarcriccaacriccristiaagriricricriccagaarreaagcristaaagcra
                                                                                                                                                                                                                                                                                                                                                               241 CATCAGCCAACCTCCCCAACAGCACTTTGCGTTTTCCTGTTGAGAGGGGGGGACTGAGAGAC
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                                                                                                                     CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                   CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTAAAACTA
                                                                                                                                                                                                                                                                                   GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
Gaps
ö
47; Indels
    Mismatches
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                                                                                          AGAGCACAGTGGGAGGACAAGGATTGCAATATAAACCCAGGCATTCGAGCCAGC-ANAG 1997
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treatment of, e.g. multiple sclerosis.
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/*tag= a
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Pred. No. 1.3e-158;
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                                                                                    This sequence represents clone 5M6 from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-ANG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field.)
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                                    Nucleic acid sequences of retrovirus called MSRV-1 multiple sclerosis or rheumatoid polyarthritis.
                                                                                                                                                                         Score 545; DB 2; 1
Pred. No. 1.3e-158;
0; Mismatches 47;
                                                                   Claim 1; Page 39-40; 83pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene of a retrovirus associated with multiple sclerosis or rheumatoid arthritis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis. The present sequence is used in the exemplification of the invention.
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                                  arthritis
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                                                                                                                                                                                                                                                                                                                                                    Garson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1329 BP; 346 A; 352 C; 288 G; 340 T; 0 U; 3 Other;
                                    sclerosis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid and their fragments having retrovirus, useful for diagnosing, preventing and/or sclerosis and/or rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                Paranhos-Baccala
naud C, Mandrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 545; DB 12;
Pred. No. 1.3e-158;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 108; 193pp; English
                                                                         Multiple sclerosis associated retrovirus
                                                                                                                                                                                                                                                                                                                                                    Jolivet-Reynaud C,
                                    ss; pol gene; retrovirus; multiple
                                                                                                                                                                                                                                                                                                                                  Bedin F,
                                                                                                                                                                                                                                96US-00756429
97US-00979847
                                                                                                                                                                                             03-APR-2002; 2002US-00114104
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92.4%;
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MSRV associated cDNA #11
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                                                                                                                                                                                                                                                                                           (INMR ) BIO MERIEUX
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                                                                                                                                                                                                                                                                                                                                    Beseme
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Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                            Human, dithp, diagnostic and therapeutic polynucleotide, diagnosis, cancer; cell proliferative disorder, autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; gastrointestinal disorder; transport disorder; connective tissue disorder; drug screening; protecome analysis; gene therapy, antisense therapy; genotyping; transgenic animal; knock in; disease model; toxicological testing; transcript imaging; growth;
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ACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATCTATTGCCTG
                                              AGAGCACAGCGGGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAGCCAGCAACAG
                                                                                                           CAACCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTCACTCTATTTCACTCT
                                                                                            CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
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JL, Yu JY, Tuason O, Yap PB, Amshey SR;
C, Liu TF, Nguyen DA, Kleefeld Y, Gerstin Ist, Lowis SA, Chen AJ, Panzer SR, Harris B;
H. Lo A, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                Human dithp growth/development-associated protein-encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 668; 591pp; English.
                                                                                                                                                                                ATTAMATCATGCAACTGCA 875
                                                                                                                                                                                                                                                                      ACC46747 standard; cDNA; 2046 BP
                                                                                                                                                          ATTAAATCTTGCAACTGAA 619
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29-MAR-2001; 2001US-0280068P.
16-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
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                                                                                                                                                                                                                                                                                                                                   (first entry)
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Dufour GE, Hillman,
Daughtery SC, Dam TC, I
Peralta CH, David MH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              development; gene; ss
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creambinant production of DITHP proteins, antibodies specific for DITHP proteins; microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein sequences; methods of screening for compounds which specifically bind a DITHP protein; and methods of sassessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP proteins may be used in the diagnosis of a wide variety of conditions including cancer and other cell proliferative disorders; autoimmune or inflammatory disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; metabolic cylesofers; neurological disorders; pastrointestinal disorders; transport disorders; and connective tissue disorders. They may also be used to screen for modulators of protein activity or sene expression. DITHP proteins can additionally be used in analysis of the proteome of a tissue additionally useful in somatic or germline gene therapy of the disorders and to induce antibodies. The dithp nucleic acids are additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of correct of antisense sequences, as a source of the generation of transgenic animal models of human disease or knock in the present sequence represents a dithp cDNA encoding a DITHP protein contains this patent did not form part of the printed specification, but was contained in electronic format directly from WIPO at essention, but was contained in electronic format directly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 540.2; DB 8;
Pred. No. 5e-157;
0; Mismatches 33;
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94.4%;
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     Score 535; DB 9; L
Pred. No. 1.7e-155;
0; Mismatches 57;
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90.8%;
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                                                              Conservative
Query Match
Best Local Similarity
Matches 562; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated or purified nucleic acid from a virus associated with multiple sclerosis and/or rheumatoid arthritis, unitiple sclerosis associated virus (MSRV)-1. The nucleic acids comprise pol, gag or reverse transcriptase genes (or their fragments) encoding the proteins or defined peptides (including immunodominant peptides.

The including are process for arthritis in a biological sample, a nucleic acid probe for the detection arthritis in a biological sample, a nucleic acid probe for the detection of a virus associated with multiple sclerosis or rheumatoid arthritis, a polypeptide exhibiting an inhibitory activity on the protectivity on the protective and an antibody directed against the MSRV-1 virus obtained by and an antibody directed against the MSRV-1 virus obtained by immunogenic agent consisting of the antigenic polypeptide defined above.

The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis. The present detecting in a biological sample, the presence of associated with multiple sclerosis or rheumatoid arthritis. The present consisting consisting of the antigenic polypeptide defined above.

The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis. The present consisting in a biological sample, the presence of actually determined MSRV-associated sequences as displayed in the main body of the post incommence is a claimed MSRV-associated sequences as displayed in the main body of the presence of or exposure to a virus accurately determined. Note: The SEQ ID numbers for the sequences as displayed in the main body of the present sequences and in the sequence listing. Consequently those sequences mentioned in the harman bank and the main bank and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuke PW;
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                                                                                                                                                                                                                                                                                         sclerosis; rheumatoid arthritis; gag; pol;
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                                                                                                                                                                                                                                                                                                                      reverse transcriptase; ribonuclease H
                                                                                                                                                                                                                                     MSRV-1 associated DNA sequence #21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 31; Page 80; 193pp; English.
                                                                                   BP.
                                                                                 ADB84403 standard; DNA; 1329
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PARAMHOS-BACCALA G.
KOMURIAN-PRADEL F.
JOLIVET-REYNAUD C.
MANDRAND B.
GARSON J A.
TUKE P W J.
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BESEME F.
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                                                                                                                                                                                                                                                                                                                                                                    Unidentified;.
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(BEDI/) (PARA/) (KOMU/) (JOLI/) (MAND/) (GARS/) (TUKE/)

Perron

(BESE/)

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bone marrow, treatment, prevention, nutrition, cytokine; immune; vaccine; cell proliferation; cell differentiation, suppressor; tumour inhibition, hematopoiesis regulator; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.
                                                                                           Secreted protein; testes; brain; blood; placenta; human; murine; thymus;
Human secreted protein AJ172_2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-1998;
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Sequence 1329 BP; 339 A; 346 C; 282 G; 332 T; 0 U; 30 Other;

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This is the human secreted protein AJ172 2 nucleotide sequence, obtained from a human adult testes CDNA library. The invention relates to secreted human and mutrine proteins. The polymocleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Detection of the levels of the proteins can be used for the caimans. Detection of the levels of the proteins can be used for the caimans. Detection of the levels of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds), cytokine and activity in large sequential activity, immune stimulating activity, tissue growth activity, activin/inhibin activity, conferenceallocked activity, and tumour inhibition activity. The invasion suppressor activity, and tumour inhibition activity. The polymucleotide sequences are also stated to be useful for gene therapy
2791 AGAGCACAGCAGGAGGACAATGATCGGGATATAAACCCAAGTCTTCGAGCCGGCAACGG 2850
                                                                          New polynucleotides encoding secreted cDNA libraries, used to develop products for the diagnosis and treatment of neoplastic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; disease diagnosis; pre-eclampsia; cancer; placental pathology; metastasis inhibition; nutritional activity; immune stimulator; haematopoiesis regulator; tissue growth; tumour inhibitor; anti-inflammatory; clone AJ172_2; ATCC_98115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.1%; Score 533.8; DB 3; Length 2946; 91.5%; Pred. No. 5.9e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein AJ172_2 polynucleotide sequence.
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98US-00175928
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTGTATCTTTAACCTCCCTTGTTAACTTTGTCTCTTCCAGAATCGAAGCTGTAAAACTA 2382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2946 BP; 858 A; 801 C; 570 G; 717 T; 0 U; 0 Other;
                                                                                                                                                                         Lavallie ER, Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding secreted proteins.
                                                                                                                                                                                                                                                                                                                                                                      Claim 13a; Page 100-101; 142pp; English.
                             97US-00976110.
98US-00080478.
98US-00175928.
                                                                                                                            (GEMY ) GENETICS INST INC.
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Treacy M;
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Merberg D,
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                                 CCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTTCCAGAATCGAAGCTGTAAAACTA
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                                                                                     ------CAAATGGAGCCCAAGATGCAGATCTAAGATCTACGCAGACCC
                                                                                                        CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                        GAAATCTCAGCTGCACAACCTCTACTACGCCCCAATTCAGCAGGAAGCAGTTAGAGCGGT
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Mismatches
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Matches 581; Conservative
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The invention relates to a protein comprising fully defined A2302 1

protein or BD127 1 6 protein. The polynucleotides are useful for
expressing recombinant proteins for analysis and are also useful as
chromosome markers or tags to identify chromosomes or to map related
chromosome markers or tags to identify chromosomes or to map related
gouste, nitrogen source and carbohydrate source. The proteins are useful
for treating various immune deficiencies and disorders (e.g. severe
combined immunodeficiency (SCID), autoimmune disorders, inflammatory
reactions (e.g. asthma), myeloid or lymphoid cell deficiencies,
caccines (SIRS), inflammatory disease, Parkinson's disease),
cosqualation disorders, inflammatory diseases (e.g. systemic inflammatory
response syndrome (SIRS), ischaemia-reperfusion injury, Crohn's disease),
anaphylaxis and hypersensitivity. Proteins are also useful for inducing
tumour immunity, for inducing bone, cartilage, tendon, ligament and/or
nerve growth or regeneration, for proliferating neural cells and for
inhibiting tumour growth. Proteins are also useful as Chemokine for
inhibiting tumour growth. Proteins are also useful as Chemokine for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2323 CCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTTCCAGAATCGAAGCTGTAAAACTA 2382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
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Bowman MR, Spaulding V, Carlin-Duckett M;
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96US-00721488
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les 581; Conservative
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Kelleher K;
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/standard_name= "Single nucleotide polymorphism"
replace(35463,C)
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replace(35318,G)
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replace(11379. .11380,AAA)
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replace(13904,G)
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replace(25444. .25446,TT)
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replace(28010,R)
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/standard_name= "Single nucleotide polymorphism"
replace(2<u>8</u>107,Y)
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/standard_name= "Single_nucleotide_polymorphism"
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replace(31808,T)
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replace(7590,A)
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replace(11004,G)
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replace(32807,C)
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replace(34531,G)
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/standard_name=
replace(9572,A)
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replace(9315,C)
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replace(1399,G)
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replace(1871. .1873,TG)
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replace (37470,G) /*tag= bj /standard_name= replace (37481,A)	/ ray- or // ray- or // replace(37499,T)	/ tag= bi /standard name= replace(40178	/"Lay=" bm /standard_name= replace(40787,A) /*tag= bn	/standard_name= replace(44582,G) /*tag=bo	/standard_name= replace(45615,A)	/standard_name= replace(46091,T) /*tag=bq	/standard_name= replace(47844,C) /*tag= br	/standard_name= replace(48013,T) /*tag= bs	/standard_name= replace(48072,A) /*tag=bt	/standard_name= replace(50802,T) /*tag= hi	/standard name=	/*tag= bv /standard_name= ' replace(53378f	/ cay=	/*tag= d /number= 2	5390483114 /*tag= e /number= 2	replace (56233,G)	/standard name= replace (56453, C)	/ rag= by /standard name= replace (59300,T)	/standard_name= replace(60998,A)	/standard_name= replace(63013,A)	/ tag- cz / standard name= replace (63293,A)	/ tay= cc / Btandard name= replace (64181,T) /**	/ standard name= replace (64191,A)	/*cag= ce /standard_name= replace(68992,C)
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170822 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAAAATTGAAGCTCTAAAACTA 170763 170702 CTGGACCGGCCTGCTAGCCCATGCTCCGATGTAATGACATCGAAGGCACCCCTCCAGAG 170643 170582 CATCGGCCATCCTCCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGTACTCAGAGAC 170523 170462 GCTTCTACCTTTAAACCCGGGGCTTGCAACTTAGCTCACACCTGACCATCAGGTAGGAA 170403 170282 CAGCAATGGCTACCATTTTTGGGTCCCCTCTCTTTGTATGGGAGCTCTGTTTTCACTCTA 170223 ä 180 240 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGC 300 360 531 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120 591 471 9 CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG 1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA 181 GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT 301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 412 AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC TATTGCCTGAGAGCACAGCGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGC 532 CGGCAACGCCAACCCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCTA 361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC-----9; Gaps /*tag= ci ...,n/ /standard name= "Single nucleotide polymorphism" replace(79395,T) /*tag= ci /standard name= "Single nucleotide polymorphism" replace(79474,G) /*tag= cl //stag= cl /single nucleotide polymorphism" replace(81065,C) /*tag= cm /*tag= cg /standard_name= "Single nucleotide polymorphism" replace(77368,G) /*tag= ch /standard_name= "Single nucleotide polymorphism" /*tag= ck /standard_name= "Single nucleotide polymorphism" replace(79992,T) Length 326014; name= "Single nucleotide polymorphism" Indels Score 532.8; DB 6; Pred. No. 1.2e-153; 0; Mismatches 52; /*tag= cf
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replace(76246,Y) Query Match
Best Local Similarity 90.5%;
Matches 583; Conservative variation variation variation variation variation variation variation 61 121 241 472 592 ઠે 셤 ò g ò qq ò . q ò g ò q ò g ò g ઠે 셤 ò g 상 점

RESULT 16

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Atandard hame= "Single nucleotide polymorphism (SNP)"
replace(50802.1)
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replace(44582,G)
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replace(28356,T)
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                                                      /standard_name=
replace(28178,R)
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/*tag= s
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3000. 323016
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replace(1871. .1873,TG)
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replace(9315,C)
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/transl_except= (pos:142261. .142263, aa:Glu)

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replace(12485. .12487,TC)
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replace(12478,A)
                                                                                                                                            Kinase; diagnosis; cancer; tissue growth abnormality; drug screening assay; cytostatic; gene therapy; human; SNP; single nucleotide polymorphism; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product= "Human kinase protein"
                                                                                                                                                                                                                                        Cocation/Qualifiers
replace(1138. .1140,GT)
                         ADQ94981 standard; DNA; 326014 BP.
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/standard_name=
replace(11004,G)
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                                                                                    (first entry)
                                                                                                                 Human kinase genomic DNA.
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3170. .
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170582 CATCGGCCATCCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGTACTCAGAGAC 170523
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                                                                                                                                                                                                                                                             170402 AGAGACCTCACTAAAATGGTAACTAGGCTAAAACAGGAGGTAAAGAATAGCCAATCATC 170343
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                                                  CATCAGCCAACCTCCCCAACAGCACTTGGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
                                                                                                                                                                             GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC-----
                                                                                                              AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                                          472 TATTGCCTGAGAGCACAGGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGC
                                                                                                                                                                                                                                                                                                                                                                        CGGCAACGCCAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of a human endogenous retrovirus envelope protein.
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(INRM ) INST NAT SANTE & RECH MEDICALE.
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99FR-00011793,
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15-SEP-1999;
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replace(56233,G)
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diabetes;

Clone; human endogenous retrovirus; genome; autoimmune disease; multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diak disseminated lupus erythematosus; pregnancy; chromosomal marker; ss

Human endogenous retrovirus

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                           protein. The specification describes a method for detecting expression of an envelope protein from a human endogenous retrovirus (HERV), in cells, of a tissue or culture. The method comprises detecting syncytia formation due to the fusogenic properties of the envelope protein. Envelope polypeptides and polynucleotides are used to produce therapeutic or prophylactic compositions, particularly for treatment of cancer, to correct defects in placental development (or other natural formation of other types of syncytia), and to promote adhesion of cells in grafts or cellular repair processes. Expression of sequences antisense to the
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                                                                                                                                                                                                                                             Length 2781;
                                                                                                                                                                                                             Sequence 2781 BP; 747 A; 770 C; 556 G; 708 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                              polynucleotide are used to prevent formation of syncytia
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                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                         Score 532.2; DB 5;
Pred. No. 1.8e-154;
0; Mismatches 43;
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ilarity 91.3%;
Conservative
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Best Local Similarity
Matches 580; Conserv
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This sequence represents clone cl.C4C5 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, theumatoid polyarthritis, disseminated lupus erythematosus, insulindependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes

New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune

disease, and abnormal or failed pregnancy

Claim 1; Page 59-60; 106pp; French

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Mallet

Mandrand B,

Bouton O,

Beseme F, Blond J, WPI; 1999-120897/10

(INMR.) BIO MERIEUX

98WO-FR001442 97FR-00008815

06-JUL-1998; 07-JUL-1997;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1136;
                                                                                                                                                                                                                                                                                                                                                                                              susceptibility to these conditions, or proximity markers of associated with this susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1136 BP; 336 A; 289 C; 241 G; 270 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 525.8; DB 2;
Pred. No. 1.1e-152;
0; Mismatches 47;
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Best Local Similarity 90.7%;
Matches 576; Conservative
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Human endogenous retrovirus W clone cl.C4C5.

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------CAAATGGAGCCCAAGATGCAGTCCAAGACTAAGATCTACCGCAGACCC
                                               CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                           618 CTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCCTGAG
                                                                                                                                               GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX25661 standard; cDNA to
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                                             fragment, which is associated with an accimmune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor I cell
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                                                                                                                                                    1038 CAACCCCCTTGGGTCCCCTCCCTTGTATGGGGGCTCTGTTTTCATGCTATTTCACTCT
                                                                                                                      CAACCCCCTTTGGGTCCCCTTCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non coding sequences of HERV-W from human genome.
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82.8%; Score 525.8; DB 3; Length 1136;
Best Local Similarity 90.7%; Pred. No. 1.1e-152;
Matches 576; Conservative 0; Mismatches 47; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1136 BP; 336 A; 289 C; 241 G; 270 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                           New nucleic acid from human endogenous retrovirus, useful e.g. for diagnosis of autoimmune disease and complications of pregnancy, contains
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gag gene; pregnancy; multiple sclerosis; T cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2782;
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Pred. No. 1.7e-151;
0; Mismatches 49;
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Local Similarity 90.4%;
es 574; Conservative
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                                 This sequence represents clone cl.PH74 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulindependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes
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                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                   Score 522.6; DB 2; Length 2782; Pred. No. 1.7e-151;
                                                                                                                                                                                                               Sequence 2782 BP; 741 A; 767 C; 565 G; 709 T; 0 U; 0 Other;
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   Claim 1; Page 60-63; 106pp; French
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designated HERV-W. The present invention describes proteins or peptides (I) having superantigen (SAg) activity comprising the ENV protein (ENV) of HERV-W, the present invention describes proteins or peptides (I) having superantigen (SAg) activity comprising the ENV protein (ENV) of HERV-W, the surface protein (SU) and transmembrane (TM) sub-units. (I) have neuroprotective activity, and can be used in: vaccines; antisensetherapy; and HERV-W SAg activity-inhibitors. (I) and encoding DNA/RNA are useful for diagnosing multiple sclerosis (MS) or HERV-W-associated disorders. (I) are also useful for identifying substances (and optionally with MS; substances capable of binding to a retroviral superantigen associated with MS; substances capable of blocking SAg activity and substances capable of blocking capable of promise of the capable of sag activity and being capable of HERV-W retroviral superantigen associated with MS; or capable of blocking saginst MS; Substances capable of blocking sAg activity, capable of blocking transcription or translation of HERV-W retroviral superantigen for use in treating or translation of HERV-W retroviral superantigen for use in treating or preventing MS; obtained using (I) are useful for the treatment and prevention of MS; (I) and nucleic acids encoding them are useful for diagnosing autoimmune disease. The present sequence encodes the
                   On the basis of the PBS t-RNA motif used for the classification of human endogenous retrovirus (HERVs) the full length endogenous provirus which was been located on the long arm of human chromosome 7 (7q21-22) has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specifically claimed envelope protein of HERV-W designated G
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                      AGAGCACAGCGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein; envelope protein; unltiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective; antisense-therapy; autoimmune disorder; ds.
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(pos:790. 792,aa:Phe)
(pos:812. 795,aa:Thr)
(pos:812. 814,aa:Thr)
(pos:818. 820,aa:Ser)
(pos:865. 864,aa:Tyr)
(pos:1174. 1176,aa:Arg)
(pos:1174. 1176,aa:Arg)
(pos:2017. 2019,aa:Lys)
(pos:2017. 2019,aa:Lys)
(pos:2017. 2019,aa:Lys)
(pos:2018. 2018,aa:Arg)
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                                                                                                                                                                                                              HERV-W envelope protein G encoding nucleic acid.
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                                                        Length 2782;
Sequence 2782 BP; 741 A; 768 C; 564 G; 709 T; 0 U; 0 Other;
                                                                                                                   Indels
                                                     82.3%; Score 522.6; DB 5; 90.4%; Pred. No. 1.7e-151; ive 0; Mismatches 49;
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                    CTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCCTGAG
                                                                                                         2493 GAAATCTCAGCTGCACAACCTCTACTACGCCCCCAATTCAGCAGGAAGCAGTTAGAGGGG
                                                                                                                                                                   241 CATCAGCCAACCTCCCCAACACACACTTGGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGAC
                                                                                                                                                                                                                                                           AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                                                                                                              421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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                                                                          181 GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                      361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
Colon adenocarcinoma related gene sequence SEQ ID NO:81.
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2000US-0234009P.
2000US-0234034P.
2000US-0234509P.
2000US-0234509P.
2000US-0234567P.
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2000US-0235082P.
2000US-0235134P.
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2000US-0209531P.
2000US-0233133P.
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20-SEP-2000;
20-SEP-2000;
20-SEP-2000;
22-SEP-2000;
25-SEP-2000;
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25-SEP-2000;
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ABL61744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying compounds which are modulators of syncytin expression. The syncytin modulators are useful in diagnosis and treatment of preeclampsia and gestational trophoblast disorders (e.g. choriocarcinoma, hydatiform mole, placental site tumour and missed/incomplete abortion). Syncytin is a human gene derived from the envelope gene of human endogenous defective retrovirus, HERV-W. The present invention is based partly on the discovery that syncytin expression is dramatically reduced in preeclampsia, and is also mis-localised to the spical syncytiotrophoblast membrane. The present sequence is human syncytin cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a compound for treating a subject with or at risk of developing preeclampsia, comprises determining whether the expression or activity of syncytin in the cell is modulated in the presence of a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTAAAACTA
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                                                                                                                                                                                                                                                                                                                                 Human; syncytin; preeclampsia; gestational trophoblast disorder; choriocarcinoma; hydatiform mole; placental site tumour; abortion; envelope gene; human endogenous defective retrovirus; HERV-W; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.5%; Score 517.4; DB 6; Length 2930; 91.4%; Pred. No. 7.4e-150; live 0; Mismatches 41; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2930 BP; 842 A; 800 C; 571 G; 717 T; 0 U; 0 Other;
       Disclosure; Page 39-42; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Syncytin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
930. .2546
/*tag= a
                                                                                                                                                    BP
                                                                                                                                                    standard; cDNA; 2930
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564; Conservative
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P-PSDB; AAE14540.
                                                                                                                                                                                                                                                                                          Human syncytin cDNA
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                                                                                                         RESULT 23
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IID AAD2

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CTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCCTGAG 37441
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                                                                                                                                                                               CATCAGCCAACCTCCCCAACAGGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 300
                                                                                                                                                                                                                                                                         AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone, human endogenous retrovirus, genome, autoimmune disease, multiple sclerosis, rheumatoid polyarthritis, insulin-dependent diabetes, disseminated lupus erythematosus, pregnancy, chromosomal marker, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
                                                                                                                                  GAAATCTCAGCTGCACAACCTCTACTACGCCCCAATTCAGCAGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                 361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGCTC
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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTTCCAGAATCGAAGCTGTAAAACTA 37333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reening for anti-neoplastic agent involves exposing cells to a chemical ent to be tested for anti-neoplastic activity, and determining a change expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Indels 12; Gaps
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Pred. No. 7.4e-149;
0; Mismatches 43; Indels 12;
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           26-5EP-2000; 2000US-0235638P.
27-5EP-2000; 2000US-0235638P.
27-5EP-2000; 2000US-0235711P.
27-5EP-2000; 2000US-0235840P.
28-5EP-2000; 2000US-0235603P.
28-5EP-2000; 2000US-023603P.
28-5EP-2000; 2000US-023603P.
28-5EP-2000; 2000US-023603P.
28-5EP-2000; 2000US-0236111P.
29-5EP-2000; 2000US-023691P.
29-5EP-2000; 2000US-0237173P.
29-6CT-2000; 2000US-0237173P.
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03-0CT-2000; 2000US-0237604P.
03-0CT-2000; 2000US-0237606P.
03-0CT-2000; 2000US-0237608P.
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Matches 564; Conservative
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Weaver Z;
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Soppet DR,
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               This sequence represents the complete sequence of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin- dependent diabetes and related pathologies) and of abnormal or susceptibility to these conditions, or proximity markers for associated with this susceptibility
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                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                ;; Score 511.4; DB 2;
;; Pred. No. 8.7e-148;
11; Mismatches 42;
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89.5%;
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Best Local Similarity 89.59
Matches 552; Conservative
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endogenous retrovirus

Human Key

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTAAAACTA
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ilarity 89.5%; Pred. No. 8.7e-148;
Conservative 11; Mismatches 42;
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Autoimmune disease; retrovirus; human endogenous retrovirus W; gag gene; pregnancy; multiple sclerosis; T cell proliferation;

Human endogenous retrovirus W (HERV-W) sequence:

(first entry)

07-NOV-2000

AAA59215;

BP

AAA59215 standard; DNA; 7582

RESULT AAAS921

Voisset C;

Mallet F,

Paranhos-Baccala G, (INMR) BIO MERIEUX

21-JAN-2000; 2000WO-FR000144.

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                                                                                                                  SGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAGAC
                                                                                                                                                                                           7324 ACATCCACCTTTAAACACGGGGCTTGCAACTTAGYTCACACCTGACCAATCAGAGGGCTC
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                               GAAATCTCAGCTGCACAACCTCTACTACGCCCCAATTCAGCAGGAAGCAGTTAGAGCGGT
                                                                                                 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGACTGAGAGAC
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                   CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                           GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Regulatory alements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immunor response, e.g. in immunotherapy. HERV-7q peptides and their coding sequences can be used in immunogenic or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was used to illustrate the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 46340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 510.6; DB 3;
Pred. No. 3.7e-147;
0; Mismatches 49;
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Best Local Similarity 90.0%;
Matches 575; Conservative
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(first entry)

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #4541 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present semience is an anathral of the present semience is any contract.
        9621 ACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTGACCAATCAGAGGAGCTC
                                                                 481 AGAGCACAGGGGGGGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                 9801 CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGAGCTCTGTTTTCATGCTATTTCACTCT
                                                                                                                                                                            CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                            ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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27-SEP-2000;
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Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducting immunological and/or neurological changes (which may be pathological or protective) curative). HERV-7q peptides can be used to improve efficiency of the immune response, e.g. in immunotherapy. HERV-7q peptides and their coding sequences can be used in immunotenic or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was used to illustrate the invention
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                                                                                                                                                                                                                                                                                                                                                              nucleic acid sequences of human endogenous retrovirus, HERV-7q, used diagnosis, treatment and prevention of autoimmune and neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to new nucleic acid sequences of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 10499;
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                                                Autoimmune disease; HERV-7q; chromosome 7q; immunotherapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.7%; Score 505.8; DB 3; ilarity 91.1%; Pred. No. 5.6e-146; Conservative 0; Mismatches 42;
                                                                                                                                                                                                                                                                 (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
               retroviral sequence HERV-7q
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                                                                                                                                                                                                                                98FR-00007920
                                                                                                Human endogenous retrovirus
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                                                               multiple sclerosis;
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Best Local Similarity
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                      n genome-derived single exon nucleic acid probes useful expression in human fetal liver.
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Sequence 102, App
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-66-678A-50
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US-09-979-847B-42
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9850, Ap 1047, Ap 1, Appli 1, Appli 1, Appli 2, Appli 24, Appli 5, Appli 3, Appli 3, Appli 854, App 854, App 854, App 854, App 854, App 854, App	DIAGNOSTIC,
Sequence Seq	EROSIS, FOR .30
US-09-621-976-9850 US-09-621-976-1047 US-08-464-051-1 US-08-464-051-1 US-08-462-498-1 US-08-462-438-2 US-09-13-9990-24392 US-09-149-476-139 US-09-247-155-42 US-09-247-155-42 US-09-247-155-42 US-09-759-359A-3 US-09-759-359A-3 US-09-759-359A-3 US-09-759-359A-3 US-09-759-358-4 US-09-671-325-854 US-09-671-325-854 US-09-671-325-854 US-09-671-325-854 US-09-671-325-854 US-09-671-325-854	AUCIA RENCE ETTE FIL AND NUCLEOTID WITH MULTIPLE SCL PURPOSES E, PLC 8-DOS #1.0, Version #1 979,847B 3-1997
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8.33 3.32 3.32 3.33 3.33 3.33 3.33 3.33 3.33 3.34 4.44 3.34 4.44 5.55 6.55	-847B-102 e 102, Application AL INFORMATION: AL INFORMATION: BESENE, BEDIN, F PARANHOS KOMMUTAN JOLIVET- MANDRAND GARSON, TILE OF INVENTION: ADDRESSE: OLI STREET: VA ADDRESSE: OLI STREET: VA COMPUTER: VA COMPUTER: VA COMPUTER: VB COMPUTER: IBM OPERATION NU FILING DATE: 22320 COMPUTER: 1EM OPERATION NU FILING DATE: 2 CLASSIFICATION NU FILING DATE: 1 CLESTRATION NI FILING DATE: 2 CLASSIFICATION IN FILING DATE: 303-8 MATION FOR SEQ ID N MATICAL
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ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.8%; Score 545; DB 4; L
ilarity 92.4%; Pred. No. 7.3e-172;
Conservative 0; Mismatches 47;
                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 39046A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-2787

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:

LENGTH: 1329 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TYPE: nucleic acid

STRANDEDNESS: single

TYPE: TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 108:

US-08-979-847B-108
                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <UNKnown>
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Best Local S:
Matches 572,
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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                                                                                                                                                                                                                                                                  CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                              GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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                                                                                                                                                                                                                                                                                                                                                     GADATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAAGCAGTTAGAGCGGT
                                                                                          CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAAGTA
                                               Gaps
                                               ö
      Length 635;
                                             0; Indels
  100.0%; Score 635; DB 4; I
100.0%; Pred. No. 3.5e-202;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAAAAA 635
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BEDIN, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 108, Application US/08979847B Patent No. 6582703 GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
    Query Match 100.
Best Local Similarity 100.
Matches 635; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-08-979-847B-108
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61 NTCANTAAAATGATNATINGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATTGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CGGCAACCCCTTTGGGTCCCCTCCCTTTGTATGGGAGCTNTGTTTTCATGCTATTTCAN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 ACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 CGGCAACCCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 CICACIAAAAIGCIAAIIAGGCAAAAAIAGGAGGIAAAAGAAAIAGCCAAICAICTAIIGC
                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: SECRETED
TITLE OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
FILING DATE:
                                                       2911 ATTAAATCTTGCAACTGCAAAAAAAAAAAAAA 2945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 36.8%; Score 233.6; DB 1; Best Local Similarity 88.1%; Pred. No. 4.1e-68; Matches 245; Conservative 1; Mismatches 32;
                              601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                            Sequence 50, Application US/08686878A
Patent No. 5708157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 498-824
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-686-878A-50
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STREET: 87
                                                                                                                                               RESULT 4
US-08-686-878A-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2383 ------CAAATGGAGCCCAAGATGCAGTCCAAGACTAAGATCTACCGCAGACCC 2430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2431 CTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCCTGAG 2490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2491 GAAATCTCAGCTGCACAACCTCTACTACGCCCCAATTCAGCAGGAAGCAGTAGAGCGGT 2550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, John M.
APPLICANT: Lavalile, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Webbergy David
APPLICANT: Mebrergy Murice
APPLICANT: Mi, Sha
CURRENT MILING DATE: 1994-10-20
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2671 ACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTGACCAATCAGAGGGGCTC 2730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTGGGAAGGTGACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 84.1%; Score 533.8; DB 3; Length 2946; Best Local Similarity 91.5%; Pred. No. 6.8e-168; Matches 581; Conservative 0; Mismatches 42; Indels 12;
                                                                                                                                            Sequence 3, Application US/09175928A Patent No. 6312921 GENERAL INFORMATION:
857 ATTAAATCATGCAACTGCA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
LENGTH: 2946
                                                                                                  RESULT 3
US-09-175-928-3
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APPLICANT: Frederic BESEME
APPLICANT: Frederic BESEME
APPLICANT: Frederic BESIME
APPLICANT: Frederic BESIME
APPLICANT: Glaucia PARNHOS-BACCALA
APPLICANT: Glaucia PARNHOS-BACCALA
APPLICANT: Glaucia PARNHOS-BACCALA
APPLICANT: Colette JOLIVET
APPLICANT: Colette JOLIVET
APPLICANT: Bernard MANDRAND
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT]
TITLE OF INVENTION: THERAPEUTIC PURPOSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 CTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 AAGGIGACIGCAICCACCICIAAACAIGGGGCIIGCAACIIAGCICACACCCGACCAAIC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 AAGGTGACCACATCCACCTTTAAGCAGGGGCTTGCAACTTAGCTCACACCCGACCAGTC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 AGGTAGTAAAGCGAGCTCACTAAAATGCTAATTAGGCTAAAACAGGAGGTAAA-CAATAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 creagagacaggacragcregarrirccraggcgacraagarrccraagacraagccraggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 CCAATCATCTATTGCCTGAGAGCACAGGGGGGGGGACAAGGATCGGGATATAAAACCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 ccaarcarcrarcrcrcagagcacacagagagagagagaraagagararaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523 CATTCGAGCCGGCAACGCCAACCCCCTTTGGGTCCCCTCTCCTTTGTATGGCCGCTCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.0%; Score 196.6; DB 4; Length 456; 84.9%; Pred. No. 1.3e-55; ive 0; Mismatches 24; Indels 23
                                                                                               Sequence 3956, Application US/09621976

Sequence 3956, Application US/09621976

Patent No. 663963

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET: 054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

SOFTWARE: Patent.pm

SEQ ID NO 9366

LENGTH: 456
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-691-563C-46
; Sequence 46, Application US/08691563C
; Patent No. 6001987
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.9
Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        583 ITCACICIAII 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 TTCACTCTATT 11
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-09-621-976-9366
                                                                                        US-09-621-976-9366/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NTCANTAAAATGATNATTNGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAGAGCACAGCGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAA 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         creacadeacadeacadacaardarcegararaaacccaagrrrngagccegcaa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGCAACCCCCTTTGGGTCCCCTTTGTATGGCCGCTCTGTTTTCACTCTATTTCAC 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RCCACATCCACCTTTAAACACGGGGNTTGCAAANAAGATNACACTTGACCAATCAGAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 ACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 279;
                                                                                                                                                                                                 APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: Mavallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: BECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/721,489
FILING DATE:
         598 TCTATTAAATCTTGCAACTGAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.8%; Score 233.6; DB 1
88.1%; Pred. No. 4.1e-68;
tive 1; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts
                                                                                                                                                          Sequence 4, Application US/08721489 Patent No. 5786465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BEOWN, SCOEL A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-824
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: cDNA
US-08-721-489-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
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Best Local Simi
Matches 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418
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1566 chadaccaacccccroccc-----rrrcacroccchaagagrrcccrcrocad 1616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1506 CAGATGGTCTTACAAATGGAACCCCAAATGAGCTCAACTATCAACTTCTACTACTGAGGACCC 1565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1735 GAAGCCAGCTGGACTTCTGGGTCGGGTGGGAGACTTTTGTGTCTAGCTAAAG 1794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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Pred. No. 3e-32;
0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,766
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PTLING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 42, Application US/08979847B; Patent No. 6582703
                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1795 GATTGTAAATGCAACAAT 1812
                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-836-2787
INPORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 1859 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 GCATCCACCTCTAAACAT
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Best Local Similarity 62.7
Matches 237; Conservative
                                                                                                                                                                                                                                                       ZIP: 22314
COMPUTER READABLE FORM:
                                                                                                                                                   CITY: Alexandria
STATE: Virginia
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-979-847B-42
                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-374-766-46
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTAGACCAACCCCTGGCCC-----TTTCACTGGCCTAAAGAGTTCCCCTCTGGAG 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1617 gacactaccactócagegcóccontrificoccontrocagaaggaaghagchagagcagh 1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTGCCCAA--TTCCCAAGAGCAGCTGGGGTGTCCCGTTTAGAGTGGGGATTGAGAGGT 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1735 GAAGCCAGCTGGACTTCTGGGTCGGGTGGGGACTTGGAGAACTTTTGTGTCTAGCTAAAG 1794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.2%; Score 128; DB 3; Length 1859; 62.7%; Pred. No. 3e-32; ive 0; Mismatches 130; Indels 1
                                                                                                                               Glaucia PARANHOS-BACCALA
Florence KOMURIAN-PRADEL
Colette JOLIVET
Bernard MANDRAND
                                     ZIP: <2.5.4.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: RC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46, Application US/09374766 Patent No. 6579526 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1795 GATTGTAAATGCAACAAT 1812
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Frederic BEDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1859 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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APPLICANT:
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US-09-374-766-46
COUNTRY:
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1735 GAAGCCAGCTGGACTTCTGGGTCGGGTGGGGACTTGGAGAACTTTTGTGTCTAGCTAAAG 1794
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Patent No. 6265211
GENERAL INNORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT FILING DATE: 1998 05-13
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 3
SEQ ID NO 5
                                                                                                                                                                                                            Sequence 4, Application US/09078294
; Sequence 4, Application US/09078294
; Patent No. 6265211
; GENERAL INFORMATION:
    APPLICANT: Choo, Kong-Hong Andy
; APPLICANT: Cancilla, Michael R.
; TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
; FILE REFERCE: Davies Col
; CURRENT APPLICATION NUMBER: US/09/078,294
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
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Best Local Similarity 67.2%; Pred. No. 1.8e-30;
Matches 213; Conservative 0; Mismatches 92
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                                                  361 GCATCCACCTCTAAACAT 378
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LENGTH: 80246
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                                                                                                                                                                                                                                                       INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1506 cagargercrracaarregaaccccaaargaecrcaacrarcaacrrcracracracaagaccc 1565
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Pred. No. 3e-32;
0; Mismatches 130; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
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SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                         PARANHOS-BACCALA, GLAUCIA
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                                                                                                                                                                             MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
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INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1859 base pairs
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                                   PERRON, HERVE
BESEME, FREDERIC
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STRANDEDNESS: single
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Best Local Similarity 62.7%;
Matches 237; Conservative
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                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
               GENERAL INFORMATION
                                                                                                                                                                                                                                                            TITLE OF
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VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
THERAPEUTIC PURPOSES
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                                                                                                                                                                                             11;
                                                                                                                                               Length 1722;
                                                                                                                                                                                          80; Indels
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APPLICATION NUMBER: US/09/374,766 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Oliff & Berridge
700 South Washington Street, Suite 300
                                                                                                                                            Score 125; DB 3;
Pred. No. 2.8e-31;
0; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Herve PERRON
APPLICANT: Frederic BESEME
APPLICANT: Frederic BESEME
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Golette JOLIVET
APPLICANT: Bernard MANDRAND
TILLE OF INVENTION: VIRAL MATERIAL AND
TITLE OF INVENTION: ASSOCIATED WITH MUT
TITLE OF INVENTION: THERAPEUTIC PURPOS
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APPLICATION NUMBER: US/08/691,563
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 58, Application US/09374766
Patent No. 6579526
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                            19.7%;
                                                                                                                                          Query Match 19.7
Best Local Similarity 69.2
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                             single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22314
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 700 South
CITY: Alexandria
STATE: Virginia
TYPE: nucleotide
                                                  linear
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APPLICANT: Herve
                          STRANDEDNESS:
                                           ; TOPOLOGY: 11;
; MOLECULE TYPE:
US-08-691-563C-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-374-766-58
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Batent No. 6001987

GENERAL INFORMATION:
APPLICANT: Herve PERRON
APPLICANT: Frederic BESEME
APPLICANT: Frederic BEDIN
APPLICANT: Florence KOWURIAN-PRADEL
APPLICANT: Florence KOWURIAN-PRADEL
APPLICANT: Colette OLIVET
APPLICANT: Colette OLIVET
APPLICANT: Per AND NOT BEDIATE
APPLICANT: PROBERT MANDRAND
APPLICANT: BEDIATE MANDRAND
APPLICANT: TOLETTE OF INVENTION: THERAPEUTIC PURPOSES
TITLE OF INVENTION: THERAPEUTIC PURPOSES
MIMMED OF SECUENCISO.
                                                                                                                                                                                               59181 CAGATGATCTTACAAATGTAACCCCAAATGAGCTCAACTAACAACTTCTGCTGAGGACCC 59240
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                                                                                                                                                                                                                                                                                                                                                                                          59241 CTGGACCGACCGCTGGCCC-----TTTCAATGGCCTAAAGAGCTCCCTCTGGAG 59291
                                                                                                                                                                                                                                                            CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
                                                                                                                                                                                                                                                                                                                                                      CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGAC 300
                                                                                                                                                                  1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59292 GACACTACCACTGCAGGGCCCCTTCTTCACCCCTATCCAGGAGGAGGTAGCTACAGCGGT
                                                                                                                         Gaps
                                                                 Score 125.8; DB 3; Length 80595;
Pred. No. 1.8e-30;
0; Mismatches 92; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563C
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: WPB 38588
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria
STARE: Virginia
; ORGANISM: Nucleotide sequence of HC-contig
US-09-078-294-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 AGGACTAGCTGGATTTC 317
                                                                 Query Match
Best Local Similarity 67.2%;
Matches 213; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 22314
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-08-691-563C-58
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966 gacactacaactigcaggcccctrrctrrigccccratccagcaggaagragcragagggg 1025
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| Sequence 24228, Application US/09513999C
| Patent No. 6783961
| GENURAL INFORMATION:
| APPLICANT: Duclert, A. APPLICANT: Duclert, A. APPLICANT: Duclert, A. APPLICANT: Duclert, A. TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| Patent No. 6783961
| FILE REPERENCE: 59.402.REG
| CURRENT FILING DATE: 2000-02-24
| PRIOR APPLICATION NUMBER: US/09/513,999C
| CURRENT FILING DATE: 1999-02-26
| NUMBER OF SEQ ID NOS: 36681
| SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CTGGACCGGCCTGCTAGCCCATGCTCGATGTTAATGACATTGAAGGCACCCCTCCCGAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               796 cccrerarrrrraaccrrcrrcraaarrrrerrrccrcrasgarcaagcra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               856 cagargercriacaaaregaaceeeaareacricaacraacaacarerreaceaagaeee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GAAATCTCCACCACACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1026 carcesccaa-arrcccaacascastresserstrestrates de de 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                               Length 1722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        80; Indels
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Pred. No. 3.9e-27;
                                                                                                                                                                                                                                                                                                                                                                               Score 125; DB 4;
Pred. No. 2.8e-31;
0; Mismatches 80;
                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-08-979-8478-54
                                                                                                         LENGTH: 1722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              TYPE: nucleotide
STRANDEDNESS: single
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90.1%;
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69.2%;
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US-09-513-999C-24228
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Best Local Similarity 69.2'
Matches 204; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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Best Local Similarity
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US-09-513-999C-24228
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LENGTH: 149
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            966 gacacracaacrigcagggccccrrcrrrgccccrarccaggaggagargraggggggg 1025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           856 CAGATGGTCTTACAAATGGAACCCCAAATGAGTTCAACTAACAACTTCTACCAAGGACCC 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG 180
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                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                        19.7%; Score 125; DB 4; Length 1722; 69.2%; Pred. No. 2.8e-31; ive 0; Mismatches 80; Indels 1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 658703-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BRENARD
GARSON, JEREMY
TUKE, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54, Application US/08979847B Patent No. 6582703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PERRON, HERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
                                                   1722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ALEXANDRIA STATE: VA
                                                                                                                                                                                                                                                                                                                                Best Local Similarity 69.2
Matches 204; Conservative
              SEQUENCE CHARACTERISTICS
                                                                     nucleotide
RDNESS: single
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                                                                                                                                                         linear
                                                                                TYPE: nucleot
STRANDEDNESS:
                                                                                                                                                     TOPOLOGY: li
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                                               LENGTH:
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Matches

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PILE REPERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION UNDER: US 60/122,487
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 21394
LENGTH: 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 CCAGATGGAGTCCATGACTAAGATCCACCGTGGACCCCTGGACCGGCCTGCTAGCCCATG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 TCAAATGAGCTCAACTCACGGCTTCTACTGAGAACCCCTGGATCCACCTGCTGGTCCTC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 CTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAATCTCAACTGCACAAACCCCT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 ------ACTAGCCTAAAAGTTCCCCTCTGGAGGACACCACAACTGCAGGGCCCCT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 ACTATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGTCATCAGCCAACCTCCCCAACAGC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 TCTTCACCCCTAACCATCAGGAAGTAGCCAGAACG---ACTGCTGCCAGTTCCCAACAGC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 TAATCAAGTGTAATCAAGGATCAAGGCCATCAAGCTGCAAATGGACTTACAAATGGAACC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 TAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTACAAATTGTTCTTCAAATGGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ATATAAACCCAGGCATTCGAGCTGGCAACAGCAGCCCCCCTTTGGGTCCCTTCCCTTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                               11.6%; Score 73.4; DB 4; Length 492; 60.1%; Pred. No. 2.3e-14; ive 0; Mismatches 96; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 443;
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TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NOMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 11057
LENGTH: 492
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Pred. No. 7.5e-14;
1; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 ACTIGGGTTTTCCTGTTGAGAGGGGGGACTGAG 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 21394, Application US/09513999C
; Patent No. 6783961
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Best Local Similarity 89.2%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 60.1
Matches 164; Conservative
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US-09-513-999C-21394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                          US-09-621-976-11057
                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                     Query Match
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APPLICANT: TOON, JI WON
APPLICANT: DARK, HAE-SOOK
APPLICANT: ANH, JONG-SEONG
APPLICANT: ANH, JONG-SEONG
APPLICANT: HA, YOUNG-JU
APPLICANT: HA, YOUNG-JU
APPLICANT: HA, YOUNG-JU
APPLICANT: HA, YOUNG-JU
APPLICANT: CHUNG, SOO-IL
APPLICANT: BREEKENCE: 98-338
CURRENT APPLICATION NUMBER: US/09/120,653D
CURRENT FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: KOPATENTI 1.71
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                                                                                                                                                                              CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
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                                                                                                                                                                                                                                65 CAAATGGTTCTCCAAATGGAGCCCCAGATGCAGTCCATGACTAAGATCTACTGCGGACCT 124
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                                                                                                              5 CTCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAGCTATAAAACTA
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           Gaps
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12.0%; Score 76.4; DB 3; Length 3910;
Best Local Similarity 61.4%; Pred. No. 8.8e-15;
Matches 178; Conservative 0; Mismatches 101; Indels 11
     11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: DIABETES-SPECIFIC ENDOGENOUS RETROVIRUS ERV-9
        2; Mismatches
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
                                                                                                                                                                                                                                                                                          CTGG-ACCGGCCTGCTAGCCC 140
                                                                                                                                                                                                                                                                                                                                            125 CTRGNACCGGMCTGCTAGCCC 145
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        127; Conservative
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US-09-621-976-11057
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US-09-120-653D-1
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190 AGGATCAAAGCCATCAAGCTACAAATGATCTTACAAATGGAACCTCAAATGAGCTCAGCT 249
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                                  APPLICANT: Glordano, J.Y.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PARTEN OF 6783961

FALEN NO. 6783961

FILE REFERENCE: 59.02.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR APPLICATION NUMBER: US 60/122,487

RIGHT FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NOS: 36681

SEQ ID NO 13878

LENGTH: 342
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Pred. No. 0.00095;
1; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 541, Application US/10140002
Patent No. 6725730
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.5%;
Local Similarity 62.4%;
les 63; Conservative 1
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: y=c or t
US-09-513-999C-13878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen
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Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or
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NAME/KEY: misc_feature
LOCATION: 88
OTHER INFORMATION: y=c
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LOCATION: 89
OTHER INFORMATION: k=g
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OTHER INFORMATION: y=c
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LOCATION: 103
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LOCATION: 277
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                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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APPLICANT:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                         INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  63 ATGGGAG--CTGTTTTCATGCTATTTCACTCTATTAAATCTKGCAACTGCA 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68.4; DB 4;
Pred. No. 2.2e-12;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BERIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <u href="https://doi.org/10.100/">doi.org/10.100/</u>
                                                                                                                                                                                                                                                                            KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JERENY
TUKE, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSES: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-08-979-847B-105
                                                                                                                                                                                            APPLICANT: PERRON, HERVE
BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1456 CAGATGGTCTTACAAATGGAACCCCA 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CAAATTGTTCTTCAAATGGAGCACCA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13878, Application US/09513999C ; Patent No. 6783961 ; GENERAL INFORMATION:
                                                                                                                             Sequence 105, Application US/08979847B Patent No. 6582703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1481 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 87.2%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 20
US-09-513-999C-13878
                                                                                           RESULT 19
US-08-979-847B-105
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF
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GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Cohen, Daniel

APPLICANT: Chumenfeld, Marta

FILE REFERENCE: GENSET.020CPI

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER PILING DATE: 1998-04-21

NUMBER: US 60/109,732

EARLIER FILING DATE: 1998-04-21

NUMBER: US 60/109,732

EARLIER FILING DATE: 1998-04-21

SEQ. ID NOS: 11796

SEQ. ID NOS: 11796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.1%; Score 38.6; DB 4; Length 47; 87.2%; Pred. No. 0.0023; Live 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 GTGACCGCACCCTTTAAACAYGGGGCTTGTAACTCAGCTCACAC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 24
CTHER INFORMATION: 99-6549-275 : polymorphic base A or
US-09-422-978-3579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: PALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
RICR APPLICATION DATA:
RAPPLICATION NUMBER: US/07/935,313
                                                                                                                               Sequence 3579, Application US/09422978 Patent No. 6537751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.2*
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo Sapiens
     456 CTGGAC 461
                                                                               RESULT 23
US-09-422-978-3579/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YOUN, JI-WON
APPLICANT: YOUN, JI-WON
APPLICANT: JUN, HEE-SOOK
APPLICANT: JUN, HEE-SOOK
APPLICANT: HA, YOUNG-UU
APPLICANT: HA, YOUNG-UU
APPLICANT: HA, YOUNG-UU
TITLE OF INVENTION: DNA and peptides of a diabetes-specific endogenous retrovirus
FILE REPERENCE: 98 3.38
CURRENT APPLICATION NUMBER: US/09/120,653D
CURRENT FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3753 crocidercicirice accesida accirricir retricir critice --- a ara a a 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        549 TITIGGICCCCCCCTTTGIAIGGCGCTCTGITTTCACTCTATTCACTCTATTAAATC 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 cccascarritiaacsircirsicaarritsi-irsiciasarricasscricaascri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 cagargererracararcaaacecegaaraarrreaacraacracrreraegagagaeae 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTGTAAAACTA 60
                                                                       APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      489 GCGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41.2; DB 4; Length 3824;
Pred. No. 0.0052;
0; Mismatches 48; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4%; Score 40.4; DB 3; Length 464; 62.7%; Pred. No. 0.0025; ive 0; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: DIABETES-SPECIFIC RETROVIRUS ENDOGENOUS ERV-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: KR 98-10108
PRIOR FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09120653D Patent No. 6365727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3809 Trecracreccada 3824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGCAACTGAAAAAA 624
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 61.8%;
Matches 84; Conservative
                             Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.73
Matches 79; Conservative
                                                    Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Kopatentin 1.71
SEQ ID NO 6
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo Sapien
US-10-140-002-541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGAC 126
                                                                                                                                                                                                                                                                                                           3824
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US-09-120-653D-6
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                                                                                                                                                                                                                                                                             SEQ ID NO 541
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                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
APPLICANT:
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US-09-218-363-3/c
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US-09-220-132-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 TCCTAGAGCATAAACCCATGTGGCCAAGTGAGATCAGCCCTCAAGGGCACATGCCAAG 283
                                                                                                                                                                                                                                                                                                                                                                                                        281 GAGAGGGGGGACTGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 GCCIAGCIGGGAAGGIGACIGCAICCACCICIAAACAIGGGGCIIGCAACIIAGCICACA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 CCCGACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAAT 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 AGCCAATCATCTATTGCCTGAGAGCACAGGGGGAGGACAAGGATCGGGATATAAACCCA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Racdoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Bernist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SEQ ID NO 539
LENGTH: 396
LENGTH: 396
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                                                                                                                                                                                                                                                                                                                          Query Match 5.9%; Score 37.6; DB 1; Length 7 Best Local Similarity 3.7%; Pred. No. 0.12; Matches 10; Conservative 154; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1082 RRRRRRRRRRRRRRATCGCAAGCTCCCTCG 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521 GGCATTCGAGCCGCCAACGCCACCCCCTTTG 552
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 539, Application US/09854133 Patent No. 6759508 GENERAL INFORMATION:
                                                                                                              TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                TOPOLOGY: linear;
IMMEDIATE SOURCE:
CLONE: pTZgpt-F18
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 25
US-09-854-133-539
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Best Local S:
Matches 87,
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Sequence 94, Application US/09220132

Sequence 94, Application US/09220132

Sequence 94, Application US/09220132

Sequence 94, Application US/09220132

GENERAL INFORMATION:

SEQUENCE 10. 656607

SEQUENCE 10. 650607

TILLE OF INVENTION: METHODS AND COMPOSITONS FOR THE DENTIFICATION AND ASSESSMENT

TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER;

TILLE REFERENCE: 07334-074001

CURRENT PAPLICATION NUMBER: US/09/220,132

PRIOR APPLICATION NUMBER: US 60/079,303

PRIOR APPLICATION NUMBER: US 60/068,821

PRIOR FILING DATE: 1997-12-24

NUMBER OF SEQ ID NOS: 191

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 94

LENGTH: 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 AGAGCGGTCATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGAC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 TGAGAGACTAGGATTTCCTAGGCCAACGAAGAATCCCTAAGCTGGGA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 KRMMWKRWYMAAAWYCMWKGKTTTYMAAAWKGRAAMKGRAAARRGSMWTYCCRSMMMWY 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 TWWWANMAMAWTTYWARKTYCMRGGSYTKRAMKGSCCYKGGGGSMWTYYWARSM 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 AGGIGACIGCAICCACCICTAAACAIGGGGCIIGCAACIIAGCICACACCGACCAAICA 412
192 TGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGTCATCAGCCAAC 251
                                                                                                                       284 gecadesadocarioradas de contra d
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                                                                                                                                                                                                                                                      252 CTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGACAGG 303
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Patent No. 6387616
GRNERAL INFORMATION:
APPLICANT: Ozelius, Laurie J.
APPLICANT: Ozelius, Laurie J.
APPLICANT: Breakefield, Kandra O.
TITLE OF INVENTION: TORSIN, TORSIN GENES, AND METHODS OF USE
FILE REFERENCE: MGH-1184pA2
CURRENT APPLICATION NUMBER: US/09/218,363
CURRENT FILING DATE: 1998-112-22
EARLIER APPLICATION NUMBER: 09/099,454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.5%; Score 35.2; DB 4; Length 1 Best Local Similarity 19.9%; Pred. No. 0.29; Matches 49; Conservative 87; Mismatches 110; Indels
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| LOCATION: (1)...(1497)

| CTHER INFORMATION: n = A,T,C or G

US-09-220-132-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|: ||
WTWMCC 513
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Gaps ö

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543 ACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCTAT 602
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Pred. No. 0.22;
0; Mismatches 37; Indels
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US-08-011-398B-1/c
Sequence 1, Application US/08011398B
Sequence 1, Application US/08011398B
Sequence 10. 5512473
Sequence 1. Application
Sequence 1. Application
APPLICANT: Roger Brent
APPLICANT: Antonia S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
TITLE OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
             APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: EST8 and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION WIMBER: US/09/621,976
CURRENT APPLICATION WIMBER: US/09/621,976
CURRENT PLIANS DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SSOFTWARE: Parent.pm
SEQ ID NO 1047
LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603 TAAATCTTGCAACTGAAAAAAAAAAAAAAA 635
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.1)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/011,398B
FILING DATE: 29 JAN 1993
CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/160001
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.2%;
Matches 56; Conservative
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 225 Franklin
CITY: Boston
STATE: Massachusetts
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: CDS
; LOCATION: 24..176
US-09-621-976-1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AACCCTCTCAGGTCACCTTCCATGCTGTGGTGGCTTTGTTCTTTCCCTCTTTGCAATAAA 62
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Pred. No. 0.17;
0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.4%; Score 34; DB 3; Length 3568; Best Local Similarity 53.6%; Pred. No. 1.3; Matches 67; Conservative 1; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PATENT PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603 TAAATCTTGCAACTGAAAAAAAAAAAAAAA 635
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EARLIER FILING DATE: 1998-06-18
EARLIER APPLICATION NUMBER: 60/050,244
EARLIER FILING DATE: 1997-06-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 9850, Application US/09621976; Patent No. 6639063; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1047, Application US/09621976; Patent No. 6639063; Patent No. FORMATION: APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                NAME/KEY: CDS

LOCATION: (994)...(1863)

NAME/KEY: misc feature

LOCATION: (1)...(3568)

COTHER INFORMATION: n = A,T,C or G

US-09-218-363-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 56; Conserv
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US-09-621-976-9850
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US-09-621-976-1047
                                                                                                                          SEQ ID NO 3
LENGTH: 3568
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US-08-011-398B-1
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0; 539 GGCAACCCCCTITGGGTCCCCTCTTTGTATGGCGCTCTGTTTTCACTCTATTTCACT 598 0; Gaps Query Match
Best Local Similarity 58.8%; Pred. No. 2.1;
Matches 57; Conservative 0; Mismatches 40; Indels

qq δ g Search completed: January 22, 2005, 19:36:55 Job time : 61.7997 secs

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22320
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                                                                                                          516.2
511.4
510.6
500.8
                                                                                                                                                                                                                                            493.2
482.6
481.4
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415.6
395.8
388.4
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Sequence 102, App
Sequence 18, Appl
Sequence 6792, Ap
Sequence 4, Appl
Sequence 108, App
Sequence 108, App
Sequence 108, App
Sequence 118, App
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Sequence 3, Appli
Sequence 3, Appli
                                                                                                                          2005, 12:12:40; Search time 344.872 Seconds (without alignments) 10579.682 Million cell updates/sec
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                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_MEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-637-565-18
US-10-719-993-6792
US-10-416-642-4
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5 US-10-114-104-108
3 US-10-087-192-910
3 US-10-114-893-134
5 US-10-016-249-3
US-09-731-231A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                           4300275 seqs, 2872944193 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-751-985-3
                                                                                     nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries
                                                                                                                                                                                                                                                                                                          IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 08
Maximum Match 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
                                                                                                                                                                                                                       US-09-319-156B-6
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                                                                                                                               January 22,
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13 525.8 82.8 1136 16 US-10-632-793-55 Sequence 25, Appl 15 522.8 82.3 283351 18 US-10-719-993-6815 Sequence 615. Appl 15 522.8 82.3 283351 18 US-10-719-993-6815 Sequence 615. Appl 16 522.6 82.3 2782 16 US-10-632-793-26 Sequence 26, Appl 18 522.8 82.3 2782 16 US-10-632-793-26 Sequence 26, Appl 18 522.8 82.3 2782 16 US-10-133-036-1 Sequence 26, Appl 20 216.2 81.3 56033 10 US-09-09-2535-1 Sequence 31, Appl 20 216.2 81.3 56033 10 US-09-09-2535-1 Sequence 31, Appl 20 216.2 81.3 56033 10 US-09-09-2535-1 Sequence 31, Appl 20 21 510.6 80.4 161334 13 US-10-087-192-166 Sequence 31, Appl 21 22 5008 78.9 285020 31 US-10-632-793-0 Sequence 31, Appl 22 495.6 78.7 2052 16 US-10-637-192-166 Sequence 1666, Appl 22 495.6 78.7 2052 16 US-10-637-192-166 Sequence 17, Appl 22 495.6 78.7 2052 16 US-10-276-772-146 Sequence 1144, Appl 22 495.6 77.7 2052 16 US-10-276-772-146 Sequence 114, Appl 22 495.6 77.7 2052 16 US-10-276-772-146 Sequence 114, Appl 22 445.7 7.7 2052 16 US-10-276-772-149 Sequence 114, Appl 23 445.2 70.3 1393 16 US-10-220-15 Sequence 11, Appl 24 445.2 70.3 1393 16 US-10-20-15 Sequence 11, Appl 24 445.2 70.3 1393 16 US-10-220-15 Sequence 11, Appl 24 445.2 70.3 1393 16 US-10-220-15 Sequence 11, Appl 24 445.2 70.3 1393 16 US-10-220-15 Sequence 289680, Se
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ALIGNMENTS

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RESULT 1

US-08-979-847-102

US-08-979-847-102

Sequence 102, Application US/08979847

Publication No. USZ003039664A1

Publication No. USZ003039664A1

GENERAL INFORMATION:

APPLICANT: PERCON, HENCE

APPLICANT: BEDIN, FREDERIC

APPLICANT: BEDIN, FREDERIC

APPLICANT: PARANDEL, FLORENCE

APPLICANT: PARANDEL, FLORENCE

APPLICANT: WANDRAND, BERNARD

APPLICANT: WANDRAND, BERNARD

APPLICANT: WANDRAND, BERNARD

APPLICANT: WANDRAND, BERNARD

APPLICANT: MANDRAND, BERNARD

APPLICANT: MANDRAND, BERNARD

APPLICANT: TUKE, PILIP

TITLE OF INVENTION: TIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS

TITLE OF INVENTION: TREAPEUTIC PURPOSES

NUMBER OF SEQUENCES: 210

CONTRESSEE: OLIFF & BERRIDGE, PLC

STREET: P.O. BOX 19928

CITY: ALEXANDRIA

STREET: P.O. BOX 19928

CONTRY: USA

COUNTRY: USA

CONTURE READABLE FORM:

MEDILM TYPE: Floppy disk

CONTURES: BALCATION NUMBER: US/08/979,847

CLASSIFICATION HOMBER: US/08/979,847

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
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ACTABABATGCTABATTAGGCABATAGGAGGTABAGABATAGCCABTCATCTATTGCCTG 480
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                                                                                                                                                                                                                                        Length 635;
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                                                                                                                                                                                                                                      100.0%; Score 635; DB 8; I 100.0%; Pred. No. 1.5e-187;
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REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INPORMATION:
TELEFHONE: 703-636-6400
TELEFAX: 703-636-6400
SERRANDENNESS: 81191-6
                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 635, Conservative
                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDN2
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US-10-114-104-102
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Sequence 102, Application US/10114104
; Publication No. US20030198647A1
; GENERAL INFORMATION:
APPLICANT PERRON, HERVE
BESEME, FREDERIC
BEDIN, FREDERIC
FREDERIC
FREDERIC
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TUKE, PHILIP
OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL!
THERAPEUTIC PURPOSES
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                                                                                                                                                                                                                                                                                                                                      COMPUTER: IEM PC Compatible
COMPUTER: IEM PC COMPUTER: DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,104
FILING DATE: 03-Apr-2002
CLASSIFICATION CANDONDATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match

100.0%; Score 635; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 635; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/979,847
PILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO: 102:
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREMY
                                                                                                                                                                                       ADDRESSEE: OLIFF & BERRIDGE,
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                   ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 635 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 102
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                  STATE: VA
                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-114-104-102
                                                                                                 TITLE
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NAME/KEY: misc feature; LOCATION: (1)...(366710); LOCATION: (1)...(366710); OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-: US-10-719-993-6792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSOCIATED WITH METHODS OF DETECTION AND USES THEREOF
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  (636 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 1695
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                                                                                                                                    AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGGTGGGAAGGTGACT
                                                                                                                  GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGCTC
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Pred. No. 2.6e-164;
0; Mismatches 42; Indels 0; G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1996 ATTABATCTTGCAACTGAAAAAAAAAAAAAAAA 2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6792, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: ALZHEIMER'S DISEASE, MET
FILE REPERENCE: CLO01496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 6792
LENGTH: 366710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 93.4%;
Matches 590; Conservative
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US-10-637-565-18

Sequence 18, Application US/10637565

Publication No. US20040043381A1

GENERAL INFORMATION:
APPLICANT: PERRON. Herve
APPLICANT: PERRON. Herve
TITLE OF INVENTION: METHODS FOR DETECTING MSRV-1 RETROVIRUS
TITLE OF INVENTION: METHODS FOR DETECTING MSRV-1 RETROVIRUS
TITLE OF INVENTION: METHODS FOR DETECTING MSRV-1 RETROVIRUS
CURRENT APPLICATION NUMBER: US/10/637,565

CURRENT PILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: US/09/890,340

PRIOR PILING DATE: 2000-02-15

PRIOR PELING DATE: 2000-02-15

PRIOR FILING DATE: 2000-02-15

PRIOR FILING DATE: 2000-02-15

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Version 3.0

SEQ ID NO 18
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                                        GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                    AGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
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                                                                                                                                                                                                                                                                                                            ATTAAATCTTGCAACTGAAAAAAAAAAAAAAA 635
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ORGANISM: MSRV-1 retrovirus
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; LOCATION: (1)..(1626)
US-10-637-565-18
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Best Local Similarity
Matches 624; Conserva
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US-08-979-847-108

Sequence 108, Application US/08979847

Publication No. US2030039664A1

GENERAL INFORMATION:
APPLICANT: BESENGE FREDERIC
APPLICANT: PARANHOS-BACCALA, GLAUCIA
APPLICANT: PARANHOS-BACCALA, GLAUCIA
APPLICANT: WOUNTALN PRADEL, FLORENCE
APPLICANT: JOLIVET-REYNAUD, COLETTE
APPLICANT: MANDRAND, BERNARD
APPLICANT: GARSON, JERRAY
APPLICANT: GARSON, JERRAY
APPLICANT: TUKE, PHILIP
ITILE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ITILE OF INVENTION: THERAPEUTIC PURPOSES
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSES: OLIFF & BERRITAED
STREET.
                                                                  1879 ACTAMAMIGCTAMITAGGCAMAMACAGGAGGTAMAGAMATAGCCAMICATCTATIGCCTG 1938
                                                                                                                                                                                                                                                                                                                                                                                                                         1939 AGAGCACAGTGGGAGGACAAGGATTGCAATATAAACCCAGGCATTCGAGCCAGC-ANAG 1997
1639 GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCAGGAAGCAGTTAGAGCGGT 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGC
                                                                                                                           301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                      421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REGISTRATION NUMBER: 30,024
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPRAKE: 703-836-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 ATTAAATCTTGCAACTG 617
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T: P.O. BOX 19928
ALEXANDRIA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                481 AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAAACG
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Publication No. US20040043452A1

GENERAL INFORMATION:

APPLICANT: INFORMATION:

APPLICANT: RAMKINAR, Jayalaxmi

APPLICANT: RAMKINAR, Jayalaxmi

APPLICANT: RAMKINAR, Jayalaxmi

APPLICANT: RAMKINAR, Jayalaxmi

TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS

FILE REFERENCE: PF-0842 PCT

CURRENT APPLICATION NUMBER: US/10/416,642

CURRENT FILING DATE: 2003-05-13

PRIOR APPLICATION NUMBER: 60/249,407

PRIOR APPLICATION NUMBER: 2000-11-15

NUMBER OF SEQ. ID NOS: 4

SOFTWARE: PERL PROGRAM
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Pred. No. 1.3e-159;
0; Mismatches 37;
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Best Local Similarity 93.8%;
Matches 579; Conservative
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COTHER INFORMATION: a, t, c,
US-10-416-642-4
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OTHER INFORMATION: Incy
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ORGANISM: Homo sapiens
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LENGTH: 2074
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                                                                                                                                                                                                                                                                                                    Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
THERAPEUTIC PURPOSES
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 85.8%; Score 545; DB 15; Best Local Similarity 92.4%; Pred. No. 2.8e-159; Matches 572; Conservative 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: WPB 39046A
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US,10/114,104
FILING DATE: 03-Apr-2002
CLASSIFICATION: «UNKNOWI»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA SEQ ID NO: 108: US-10-114-104-108
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1329 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 108: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                      COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
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                                                                                                                                                                                              Length 1329
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                                                                                                                                                                                          85.8%; Score 545; DB 8; I 92.4%; Pred. No. 2.8e-159; Live 0; Mismatches 47;
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BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREMY
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                 SEQUENCE CHARACTERISTICS:
LENGTH: 1329 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                Best Local Similarity 92.4
Matches 572; Conservative
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US-10-114-104-108
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APPLICANT: Bacobs, Kenneth
APPLICANT: Bacobs, Kenneth
APPLICANT: Bacobs, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Bound.
APPLICANT: Bounding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Genetics Institute, Inc.
APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                       CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATT 593
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Pred. No. 1.3e-155;
0; Mismatches ,42;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 134, Application US/10114893
Publication No. US20020193567A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.5%;
Matches 581; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-114-893-134
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                                      CAACCCCTTTGGGTCCCCTCCCTTTGTATGGCGCTCTGTTTTCACTCTATTTCACTCT 600
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     AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MOTERATION:
APPLICANT: Bragelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OANCER
FILE REFERENCE: 529452000122
CURRENT PELLING NOWHER: US/10/087,192
CURRENT PELLING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
NUMBER OF SEQ ID NOS: 2059
SEQ ID NO 910
LENGTH: 21646
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 910, Application US/10087192; Publication No. US20020182586A1; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-910
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Best Local Similarity 94.8
Matches 562; Conservative
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ORGANISM: Homo sapiens
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US-10-087-192-910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09731231A
Patent No. US20020082189A1
GENERAL INFORMATION:
TATLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: UNMBER: US/09/731,231A
CURRENT APPLICATION UNMBER: US/09/731,231A
CURRENT PILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 326014
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OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Human
FRATURE:
NAME/KEY: misc_feature
LOCATION: (1)._.(326014)
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APPLICANT: Jacobs, Kenneth
APPLICANT: LaVallie, Edward R.
APPLICANT: LaVallie, Edward R.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Mi Sha
APPL
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AGAGCACAGCAGGAGGACAATGATCGGGATATAAAACCCAAGTCTTCGAGCCGGCAACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10016249; Publication No. US20030100053A1; GENERAL INFORMATION:
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Best Local Similarity
Matches 581; Conserv
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170402 AGAGAGTCACTAAAATGGTAACTAGGTAAAACAGGAGGTAAAGAATAGCCAATCATC 170343
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                         170522 AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAGGCTGGGAGGTGACT 170463
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                                                                                                                                                                                        TATTGCCTGAGAGGACAGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGC 531
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1 Sequence 25, Application US/10632793

2 Sequence 25, Application US/10632793

3 Publication No. US20040048298A1

3 GENERAL INFORMATION:

4 APPLICANT: PARANHOS-BACCALA, Glaucia

APPLICANT: WALLET, Francois

APPLICANT: WALLET, Francois

APPLICANT: VOISSET, Cecile

7 TILE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT

7 TILE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT

7 TILE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT

7 TILE OF INVENTION NUMBER: US/10/632,793

7 CURRENT FILING DATE: 2001-10-22

7 PRIOR FILING DATE: 2001-10-22

7 PRIOR FILING DATE: 2000-01-21

7 PRIOR FILING DATE: 1999-01-21

7 NUMBER OF SEQ ID NOS: 33

7 SOFTWARE: Patentin Version 3.1

7 SEATHANE: PATENTIN VAISE
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301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGACT
                                                                                                                          AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
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                                                              GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC-----
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Best Local Similarity 90.7
Matches 576; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CRGANISM: Homo sapiens
US-10-632-793-25
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Sequence 3, Application US/10751985

Publication No. US20040126861A1

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al.

APPLICANT: GUEGLER, Karl et al.

TITLE OF INVENTION: ACID MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/10/751,985

CURRENT APPLICATION NUMBER: US/10/751,985

CURRENT FILING DATE: 2004-01-07

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTHER: 226014
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          AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 360
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Best Local Similarity 90.5%; Pred. No. 2.4e-154;
Matches 583; Conservative 0; Mismatches 52; Indels 9; G
                                                                          361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC-
                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (1)...(326014)
CTHER INFORMATION: n = A,T,C or G
US-10-751-985-3
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ORGANISM: Homo sapiens
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US-10-751-985-3/c
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Sequence 6815, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REPERENCE: CL001496
; CURRENT APPLICATION UNMER: US/10/719,993
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT PILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SEQ ID NO 6815
; SEQ ID NO 6815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1777203 CAATGTTAATGACATGGAAGGCACCCTTCCGGAGGAAATCTCAACTACACACCACTACT 1777262
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                                                                                                                                                                                                                                                                                                                                                                175341 GTATGGGAGCTCTGTTTTCA--CTGTTTCACTCTATTAAATCTTGCAACTGCAAAAAGA 175398
                                                                                                                                                    175165 CAACTTAGCTCACAC———CCAACCAGAGAGTTCACTAAAATGCTAATTAGGCAAAAATA 175220
                                                                                                                                                                                                                            175045 TGGGTTTTCCTGTTGAGAGAGGGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCCGA 175104
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                                                                  175105 CTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACCGCATCCACCTTTAAAACACGGGGCTTG
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                                                                                                                  CAACTTAGCTCACCCCGACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAAATA
                                                                                                                                                                                           27 GITIGICICITCCAGAATCAAAACTGTAAAACTACAAATTGTTCTTCAAATGGAGCACCA
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Pred. No. 7.6e-151;
1; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 93.4%;
Matches 568; Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: misc feature
LOCATION: (1)...(198009
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US-10-719-993-6815
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LOCATION: (1)...(283351)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7065, Application US/10719993
| Publication No. US20040265849A1
| GENERAL INFORMATION:
| APPLICANT: CARCILL, Michele et al. |
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH |
| TITLE OF INVENTION: ALZHRIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF |
| FILE REFERENCE: CL001496 |
| CURRENT APPLICATION NUMBER: US/10/719,993 |
| CURRENT FILING DATE: 2003-11-24 |
| NUMBER OF SEQ ID NOS: 55342 |
| SOFTWARR: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 7065
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                                                                                 858 ACATCCACCTTAAAACACGGGGCTTGCAACTTAGTTCACACCTGACCAATCAGAGAGCTC 917
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                       CGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAGAC 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATCAGAGGTC
                                                                                                                                                                                                            ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                    AGAGCACAGCGGGGGGCACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGGAGTCCATGACTAAGATCCACCGTGGACCCCTGGACCGGCCTGCTAGCCCATGCTC
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Length 283351;
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93.4%; Pred. No. 3e-151;
ive 1; Mismatches 33; Indels
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Matches 568; Conservative
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ORGANISM: Homo sapiens
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US-10-719-993-7065
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2386 GGTCGGCCAACTCCCCCAACAGCACTTTCCTGTTGAGATGGGGGACTGAGAGAC 2445
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               421 ACTADAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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                                                    AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
241 CATCAGCCAACTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGACTGAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                 ## Sequence 1. Application US/10133036

## Sequence 1. Application US/10133036

## Sequence 1. Application No. US20040054133A1

## GENERAL INFORMATION:

## APPLICANT: Connead, Bernard

## PILE REPERENCE: 23135-507

## FILE REPERENCE: 23135-507

## CURRENT FILING DATE: 2002-04-26

## CURRENT FILING DATE: 2000-10-30

## NUMBER OF SEQ ID NOS: 21

## SEQ ID NO 1

## SEG ID NO 1

## ILENGTH: 2782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.0%; Score 521; DB 16; Length 2782; Best Local Similarity 90.2%; Pred. No. 1.3e-151; Matches 573; Conservative 0; Mismatches 50; Indels 12
                                                                                                                                                                                                                                                                                                                                             601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAA 635
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ORGANISM: Human endogenous retrovirus
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US-10-133-036-1
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Sequence 26, Application US/10632793

Publication No. USCO40048298A1

SEGUENCE A. MO. USCO40048298A1

APPLICANT: PARANHOS-BACCALA, Glaucia

APPLICANT: PARANHOS-BACCALA, Glaucia

APPLICANT: WALLET, Francois

APPLICANT: VOISSET. Cecile

TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT

TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT

TITLE OF INVENTION: AUTOIMMUNE US/20/469,927

PRIOR APPLICATION NUMBER: US/20/469,927

PRIOR PLING DATE: 2000-11-22

PRIOR PLING DATE: 2000-01-21

PRIOR FILING DATE: 1999-01-21

NUMBER OF SEQ ID NOS: 33

SOFTWANDER OF SEQ ID NOS: 33

SOFTWANDER OF SEQ ID NOS: 33
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Pred. No. 4e-152;
0; Mismatches 49; Indels 12; Gaps
                         CGAAGAATCCCTAAGCTGGGAAGGTGACTGCATCCACCTCTAAACATGGGGGCTTG
                                                                                                                                 507 GGGATATAAAACCCAAGGCATTCGAGCCGGCAACGGCAACCCCCTTTGGGTCCCCTCTTT
                                                                               CAACTTAGGTGAGAGCGAACGAATGAGAGGTGACTAAAATA
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Best Local Similarity 90.4%;
Matches 574; Conservative 0
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SEQ ID NO 26
LENGTH: 2782
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US-10-632-793-26
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US-10-632-793-26
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Sequence 81, Application US/09873367C

Sequence 81, Application US/09873367C

Publication No. US20030165839A1

GENERAL INFORMATION:

APPLICANT: Soppet, Daniel

APPLICANT: Badress, Gregory

APPLICANT: Badress, Meena

APPLICANT: Baner, Meena

APPLICANT: Carter, Kenneth

ITILE OF INVENTION: Carcer Gene Determination and Therapeutic Screening Using

ITILE OF INVENTION: Signature Gene Sets

ITILE OF INVENTION: Signature Gene Sets

ITILE OF INVENTION NUMBER: US/09/873,367C

CURRENT FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: U.S. 60/236,891

PRIOR APPLICATION NUMBER: U.S. 60/236,891

PRIOR PILING DATE: 2000-09-29

PRIOR PILING DATE: 2000-09-29

PRIOR PILING DATE: 2000-11-01

PRIOR PILING DATE: 2000-11-01

NUMBER OF SEQ ID NOS: 1067

SOOTHANDE: APPLICATION NUMBER: U.S. 60/245,084

PRIOR PILING DATE: 2000-11-01

NUMBER OF SEQ ID NOS: 1067

SOOTHANDE: APPLICATION NUMBER: U.S. 60/245,084
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                                             1553 cercesceaecrecedadacacarriaserrirecrerreagaresecedereagae 2612
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Pred. No. 1.6e-149;
0; Mismatches 43;
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Best Local Similarity 91.1%;
Matches 564; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Keith, Jr., James C.
APPLICANT: Mi. Sha.
Applicant: Mi.
                                                                                                                                                        2506 ACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTGACCAATCAGAGAGCTC
                                                                                                                                                                                                                                                                ACTAAAATGCTAATTAGGCAAAGGACAGGAGGTAAAGAAATAGCCAATCATTTATTGCCTG
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                        AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                           361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATCAGAGGTC
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Pred. No. 1.7e-150;
0; Mismatches 41; Indels 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 18
US-09-902-535-1
Sequence 1, Application US/09902535
; Patent No. US20020102530A1
; GENERAL INFORMATION:
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Best Local Similarity 91.4%;
Matches 564; Conservative
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; LOCATION: (930)...(2546)
US-09-902-535-1
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (4261)..(4261)
OTHER INFORMATION: n = a or g or c or t/u
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LOCATION: (2213)..(2213)
OTHER INFORMATION: n = a
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NAME/KEY: misc_feature
LOCATION: (3787)..(3787)
OTHER INFORMATION: n = a
                                    LOCATION: (130\overline{9}) .. (1309)
OTHER INFORMATION: n = a
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LOCATION: (2398)..(2398)
OTHER INFORMATION: n = 8
           FEATURE:
NAME/KEY: misc feature
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Sequence 30, Application US/10632793

Publication No. US20040048298A1

GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: WALLET, Francola
APPLICANT: WOISSET, Cecile
TITLE OF INVENTION: AUTOHMUNE DISEASE, LABELING METHOD AND REAGENT
TITLE OF INVENTION: AUTOHMUNE DISEASE, LABELING METHOD AND REAGENT
TITLE OF INVENTION: AUTOHMUNE DISEASE, LABELING METHOD AND REAGENT
TITLE OF INVENTION: AUTOHMUNE DISEASE, LABELING METHOD AND REAGENT
TITLE OF INVENTION: AUTOHMUNE US/10/632,793

CURRENT FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 1999-01-21

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATCHTION NUMBER: FF 99/0088

PRIOR FILING DATE: 1999-01-21

NUMBER OF SEQ ID NOS: 33

LENTHEN: 582 ID NO 30

LENTHEN: 582
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                                                                     CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGACTGAGAGAC
                                                                                                                                                       AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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                                                      GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
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LOCATION: (198).
OTHER INFORMATION: n = a 01
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (307).
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NAME/KEY: misc feature
LOCATION: (355)..(355)
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US-10-632-793-30
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                                                                1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
                                   12;
 DB 16; Length 7582;
Query Match

80.5%; Score 511.4; DB 16; Length
Best Local Similarity 89.5%; Pred. No. 2e-148;
Matches 552; Conservative 11; Mismatches 42; Indels
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7203

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100131 TATCGCCTGAGAGCACAGCGGGAAGGACAATGATCGGGATATAAACCCAGGCATTCAAGC 100072
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                                                                    Indels
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APPLICANT: Brgelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FEASTS FOR WINDOWS Version 4.0
SEQ ID NO 1666
LENGTH: 285020
                                                                                                                             592 TITCACICIAITAAAICITGCAACIGAAAAAAAAAA 630
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                                                                                                                                                                                                                                                                          Sequence 1666, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
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US-10-087-192-1666
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FEATURE:
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US-10-087-192-1666
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7504 CAACCCCTTTGGGTCCCCTCCCTTTGTATGGGAGCTCTGTTTTCATGCTATTTCACTCT 7563
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APPLICANT: Mortals, David W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 730
LENGTH: 161334
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                                                                                                                                                                                      ; Sequence 730, Application US/10087192; Publication No. US20020182586A1; GENERAL INFORMATION:
                                                                    ; LOCATION: (1)...(161334)
; OTHER INFORMATION: n = A,T,C or
US-10-087-192-730
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                                                                                                                                               RESULT 21
US-10-087-192-730/c
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APPLICANT: MALLET, Francois
APPLICANT: VOISSET, Cecile
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/10/632,793
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Pred. No. 5.2e-145;
0; Mismatches 54; Indels 19;
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D IN HEART, SIGNAL = 5.4
D IN HEART, SIGNAL = 5.9
D IN BT474, SIGNAL = 5.9
D IN BT714, LYUER, SIGNAL = 4.9
D IN BYDLY LYUER, SIGNAL = 6.7
D IN BRAIN, SIGNAL = 6.7
D IN BND MARKOW, SIGNAL = 6.2
D IN BONE WARKOW, SIGNAL = 6.3
D IN LUNG, SIGNAL = 3.9
D IN HELA, SIGNAL = 7.2
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      OTHER INFORMATION: ENOTHER INF
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NUMBER OF SEQ ID NOS: 49117
SOFWARE: Annomax Sequence Listing Engine SEQ ID NO 4444
EQ ID NO 4444
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ORGANIEM: Homo sapiens
PERTURES:
OTHER INFORMATION: MAP TO AC002346.1
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993 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAGCTGTAAAACAA 1052
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Publication No. US20040072154A1
GENERAL INFORMATION:
APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71111/RS/DCF
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                  Score 493.2; DB 16;
Pred. No. 5.3e-143;
0; Mismatches 43;
  PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUSCOM
SEQ ID NO 678
LENGTH: 2052
                                                                                                                                                                                                Query Match
Best Local Similarity 91.2%;
Matches 549; Conservative
                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-678
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US-09-997-722-148
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APPLICANT: Hypeq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                             CTACAAATGGAGCCCAAGATGCAGTCCAAGACTAAGATCTACGCAGACCCCTGGACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGTTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCCTGAGGAAATCTCA
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Pred. No. 1.2e-143;
0; Mismatches 44;
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US/09/869,927
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: PCT/FR00/00144
PRIOR FILING DATE: 2000-0.-21
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 28
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Publication No. US20040053245A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                78.0%;
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Matches 522, Conservative
                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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US-10-276-774-678
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27 GTTTGTCTTCCAGAATCAAAACTGTAAAACTACAAATTGTTCTTCAAATGGAGCACCA
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; OTHER INFORMATION: Incyte ID No. US20040048253A1 LG:429446.1:2000FEB18
US-10-220-120-15
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Best Local Similarity 89.1%; Pred. No. 1.7e-139;
Matches 534; Conservative 0; Mismatches 56; Indels 9;
                                                                                               HILLMAN, Jennifer L.
JONES, Anissa L.
LIU, TOMMY F.
ROSEBERRY, Ann M.
ROSEN, Bruce H.
RUSSO, Frank D.
STOCKDREHER, Theresa K.
                                                                                                                                                                                                               DAFFO, Abel
WRIGHT, Rachel J.
YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRATCHER, Shawn R.
CHEN, Wensheng
COHEN, HOWARG J.
                                                                  FONG, Willy T.
GREENAWALT, Lila B.
   DAM, Tam C.
DANIELS, Susan E.
DUFOUR, Gerard E.
FLORES, Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                          DB 11; Length 22436;
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76.0%; Score 482.6; DB 11; Length
Best Local Similarity 87.6%; Pred. No. 3.4e-139;
Matches 565; Conservative 0; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/10220120; Sequence 15, Application No. US20040048253A1; GENERAL INFORMATION: APPLICANT: INCYTE GENOMICS, INC.; APPLICANT: PANZER, Scott R. APPLICANT: SPIRO, Peter A. APPLICANT: SPIRO, Peter A. APPLICANT: SPIRO, Michael S. APPLICANT: CHAUUP, Michael S. APPLICANT: CHAUUP, Michael S. APPLICANT: CHENG, Alice APPLICANT: CHENG, Alice APPLICANT: AMSHEY, Steven A.; APPLICANT: AMSHEY, Stefan
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: Patentin version 3.1
SEQ ID NO 148
LENGTH: 22436
                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-09-997-722-148
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APPLICANT: CHEN, Wenseleng
APPLICANT: CHEN, Wenseleng
APPLICANT: COERN, Howard J.
APPLICANT: HODGSON, David M.
APPLICANT: LINCOLN, Stephen E.
TITLE OF INVENTION: SECRETORY MOLECULES
FILE REFERENCE: PT-1134 PCT
CURRENT APPLICATION NUMBER: US/10/204,887
CURRENT FILING DATE: 2002-08-21
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-02-24; 2000-05-16; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-1
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                                                                                                         430 CTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAAATCATCTATTGCCTGAGAGCACAG 489
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379 GGGGCTTGCAACTTAGCTCACACCGACCAATC-----AGAGAGCTCACTAAAATG
                                                                                                                                                                                                                         490 CGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAACCCCCT
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Publication No. US20030124569A1
GENERAL INPORMATION:
APPLICANT: INCTE GENOMICS, INC.
APPLICANT: SPIRO, Peter A.
APPLICANT: SHAH, Purvi,
APPLICANT: SHAH, Purvi,
APPLICANT: CHAUDP, Michael S.
APPLICANT: CHAUDP, Michael S.
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D'SA, Steven A
AMSHEY, Stefan
DAHL, Christopher R.
DAM, Tam C.
DANIELS, Susan E.
DUFOUR, Gerard E.
PLORES, Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROSEN, Bruce H.
RUSSO, Frank D.
STOCKDREHER, Theresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WRIGHT, Rachel J.
YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRATCHER, Shawn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FONG, Willy T. GREENAWALT, Lila B. HILLMAN, Jennifer L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JONES, Anissa L.
LIU, Tommy F.
ROSEBERRY, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAFFO, Abel
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SEQ ID NO 10
LENGTH: 1564
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1377 CTTCTTCAGTTTGTCTCTTCCAGAATCAAAGCTATAAAACTACAAATGGTTCTCCAAATG 1436
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                                TGAGTTTTCCTGTTGAGGGGGAGAACTGAGAGACAGGACTAGCTGGTTTTCCCAGGCCAA 420
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                                                                                                            CGAAGAATCCCTAAGCTAGCTGGGAAGGTGACTGCATCCACCTCTAAACATGGGGGCTTG 386
                                                                                                                                                                                                                         CAACTTAGCTCACACCCGACCAATCA-----GAGAGCTCACTAAAATGCTAATTAG 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAACCCCTTTGGGTCC 557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCTTAAATCTTGCAACT 616
                                                                                                                                               CTAAGAATCCCTAAGCCTATCTGGGAAGGTGACCGTATCCCACCTTTAAACATAGGGCTTG
                                                                                                                                                                                                                                                               TGGGTTTTCCTGTTGAGAGGGGGACTGAGACAGGACTAGCTGGATTTCCTAGGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1148, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESERRCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE:
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NO 1148
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CRGANISM: Homo sapiens
US-10-104-047-1148
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US-10-104-047-1148
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CURRENT APPLICATION NUMBER: US/10/220,120

CURRENT PILING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: 60/184,773; 60/184,698; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,777; 60/184,776; 60/184,777; 60/184,777; 60/184,776; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 TCCACCGTGGACCCCTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGAAG 166
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OTHER INFORMATION: Incyte ID No. US20040048253A1 LI:351965.1:2000FEB01
FEATURE:
                                                                                                                                                                                                                                                   APPLICANT: WRIGHT, Rachel J.
APPLICANT: YAP, Pierre E.
APPLICANT: YU, Jimmy Y.
APPLICANT: YU, Jimmy Y.
APPLICANT: BRATCHER, Bhan L.
APPLICANT: BRATCHER, Bhan R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: HODGSON, DAVIG M.
APPLICANT: HODGSON, Stephen E.
APPLICANT: JACKSON, Stephen E.
APPLICANT: JACKSON, Stuart
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: PT. 1113 PCT.
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                                                                                                                                                                                                              STOCKDREHER, Theresa K.
HILLMAN, Jennifer L.
JONES, Anissa L.
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LOCATION: 120, 765
COTHER INFORMATION: a, t, C,
US-10-220-120-17
                                                                       LIU, Tommy F.
ROSEBERRY, Ann M.
                                                                                                                                      ROSEN, Bruce H. RUSSO, Frank D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 GAATCAAAACTGTAAAACTACAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 GAGAGGGGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAA 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGAAGGCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAG 220
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                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030124569A1 LI:813218.1:2000FEB01
FEATURE:
NAME/KEY: unsure
LOCATION: 307, 317-318, 335, 918, 921, 943, 1011
OTHER INFORMATION: a, t, c, g, or other
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70.7%; Score 449; DB 15; Length 1564;
Best Local Similarity 90.9%; Pred. No. 3e-129;
Matches 490; Conservative 0; Mismatches 45; Indels 4
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Publication No. US20040048253A1
GENERAL INFORMATION:
APPLICANT: PANZER, Scott R.
APPLICANT: SPIRO, Peter A.
APPLICANT: BANVILLE, Steven C.
APPLICANT: GHALP, Michael S.
APPLICANT: GHALP, Michael S.
APPLICANT: CHANG, Simon C.
APPLICANT: CHANG, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D'SA, Steven A.
AMSHEY, Stefan
DAHL, Christopher R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAHL, Christopher
DAM, Tam C.
DANIELS, Susan E.
DUFOUR, Gerard E.
FLORES, Vincent
FONG, Willy T.
       ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                 ; OTHER INFORM
US-10-204-887-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
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	541 CTGTTTTCACTCTATT 556	541	qq
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_	481 CCAAGCATTCGAGCCAGCAGCAGCTGCCCCTTTGTGTCCCCTCCTTTGTATGGGAGCT 540	481	qa
~	CCAGGCATTCGAGCCGCAACGGCAACCCCTTTGGGTCCCCTCTTTTGTATGGGCGCT 577	518	ò
_	AATAGCCAATCATCTATCGCCTGAGAGCACAGCAGC	421	qa
~	458 AATAGCCAATCATCTATTGCCTGAGAGCACAGCGGAGGACAAGGATCGGGATATAAAC 517	458	ò
_	CAATCAGGTAGTAAAGAGAGCTCACTAAAATGCTAATTAGGCAAAAACAGGAGGTAGAGA 420	361	qa
_	CAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGAAAAGA 457	407	ò
_	CTGGGAAGGTGACCGCGTCTACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCCCAAC 360	301	đ
	CTGGGAAGGTGACTGCATCCACTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGAC 406	347	δ
_	241 GGGGACTGAGAGAGAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCTAG 300	241	ą

Search completed: January 22, 2005, 20:08:26 Job time : 355.872 secs

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January 22, 2005, 12:01:19; Search time 1891.54 Seconds (without alignments) 12232.983 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

65645750 Total number of hits satisfying chosen parameters:

32822875 seqs, 18219865908 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

gb_est1:: gb_est2:: gb_est3:: gb_est4:: gb_est6:: gb_gs81:: gb_gs81::

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	-:	Description	BC030968 Homo sapi	CR605851 full-leng	CR617248 full-leng	CR622175 full-leng	BI087886 602852690	CR625046 full-leng		BX365066 BX365066	BX357208 BX357208		BX337769 BX337769	BX378303 BX378303	σ		9	AW971553 EST383642	CN645411 ILLUMIGEN	BC026287 Homo sapi	AG033781 Pan trogl	AI598135 tn14a10.x	BE732673 601571305	BI963185 ie57c10.x	BX380176 BX380176	AG058970 Pan trogl
SUMMARIES	;	ei .	BC030968	CR605851	CR617248	CR622175	BI087886	CR625046	CN272394	BX365066	BX357208	CR613169	BX337769	BX378303	AG121669	AA781423	BX439636	AW971553	CN645411	BC026287	AG033781	AI598135	BE732673	BI963185	BX380176	AG058970
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	:	Match Length DB	1160	2748	2749	2500	771	2748	719	1071	758	2716	966	1058	689	494	1019	522	870	1500	653	490	440	543	996	651
a	Query	Match	78.6	77.6	77.0	76.9	76.5	76.4	74.1	73.8	73.5	73.2	71.5	71.4	71.0	68.8	68.5	68.1	67.7	8.99	9.99	65.5	62.6	62.4	62.2	62.2
	(Score	498.8	492.8	488.8	488	485.6	485	470.6	468.6	466.6	464.6	454.2	453.6	450.8	437	435	432.4	430.2	424	423	415.8	397.4	396	395.2	394.8
	Result	No.	H	7	e	4	S	9	7	ω	ი ს	10	c 11	•	c 13	c 14	c 15	c 16	17	18	c 19	c 50	21	c 55	c 23	C 24

AG126669 Pan trog1 AG066901 Pan trog1 AA837267 od26b10.8	AQ892947 HS_3131_B A1128526 qc61h10.x A1393478 tg45g04.x A2036800 par froct			. •	AA552941 nk61a10.8 AA426511 zw02e05.r AG133542 Pan trog1 AG091649 Pan trog1	1813
AG126669 AG066901 AA837267	AQ892947 AI128526 AI393478	AW511366 BX481837 Allianses	CB231128 AI074704	AI128496 AG030228 AIS70707	AA552941 AA426511 AG133542 AG091649	CB069106
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393.2 393 392.6	386.8	384.2	369.6	364.2 360.6 359.8	359.8	355
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ALIGNMENTS

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 9100 GEVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
191 9100 GEVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
192 strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Li (bases 1 to 2748)
Li W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 ACTAMANTGCTMATTAGGCAMMANTAGGAGGTMANGAMANTAGCCANTCATCTATTGCCTG
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full-length cDNA clone CS0DE012YJ24 of Placenta of Homo sapiens
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                                                                                                                                                                                                                                   Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitroGen Corporation 1600
Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.6%; Score 492.8; DB 3; 90.9%; Pred. No. 2.3e-131; iive 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .2748
/organism="Homo sapiens"
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/db_Xref="taxon:9606"
/clone="CSODEDIZY124"
/tissue type="placente"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                          CR605851.1 GI:50486658
HTC; CNSLT CDNA.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                     (bases 1 to 2748)
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                             human
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Best Local Si
Matches 540;
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                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
       DEFINITION
                                                                                                                                                                                                              TITLE
JOURNAL
REMARK
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AUTHORS
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AUTHORS
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                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plates 41 Row: m Column: 10 This clone has the following problem: retained intron. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAATCTCA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGCACAACCTCTACTACGCCCCCAATTCAGCAGGAAGCAGTTAGAGCGGTCGTCGGCCA 761
       cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAACCCCT
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Pred. No. 3.4e-133;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
mol_type="makha"
db xref="taxon:9606"
/clone="IMAGE:4724433"
/clone="IMAGE:4724433"
/clone Tib="NIH MGC_79"
/lab_nost="Dacenta"
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92.6%;
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Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
                                                                                                                                                                                                             2639
                 2460 AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACC 2519
                                                                                                     420
                                                                                                                                                                   480
                                                                                                                                                                                                                                                       481 AGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LK62/1/5
full-length cDNA clone CS0DI051YM13 of Placenta Cot 25-normalized of Homo sapiens (human).
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                  1580 ACTAAATGCTAATTAGGCAAAGACAGGAGGTAAAGAAATAGCCAATCATTGCCTG
                                                                                                                                                                     ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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                                                                                   361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Gaps
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                                                                                                                                                                                                                                                                                                                                        541 CAACCCCCTTTGGGTCCCCTTCGTATGGGCGCTCTGTTTTCACTCT 590
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Mammalia, Eutheria, Primates, Catarrhini, Hor
1 (bases 1 to 2500)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Unpublished
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Pred. No. 5.5e-130;
0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 2500
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="cS0D1051YM13"
/tissue_type="Placenta Cot 25
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CR622175.1 GI:50502982
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Best Local Similarity 91.1%;
Matches 534; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTC; CNSLT cDNA.
Homo sapiens (human)
Homo sapiens
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301
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) and Extrand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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full-length cDNA clone CS0D1022YJ18 of Placenta Cot 25-normalized
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Li W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                 2635 AGAGCACAGCAGGAGGACAATGATCGGGATATAAACCCAAGTCTTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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                                                                               CAACCCCTTTGGGTCCCTTTGTATGGCGCTCTGTTTTCACTCTTTT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.0%; Score 488.8; DB 3; Length 2749; larity 90.8%; Pred. No. 3.3e-130; Conservative 0; Mismatches 42; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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/clone="CSODI022YJ18"
/tissue_type="placenta_Cot_25-normalized"
/plasmid="pCMVSPORT_6"
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                                                                                                                                                                                                                                                                        of Homo sapiens (human)
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LRDZDU46 21-JUL-2004 ENNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI044YK06 of Placenta Cot 25-normalized of Homo sapiens (human).
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                                                                                                                                                                                                 CTGGACCGGCCTGCTAGCCCCATGTTAATGACATTGAAGGCACCCCTCCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 GCCAACCCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTTTTCACT
                                                                                                                                                                                                                   GAAAICICAACIGCACAAACCCCIACIATIAGCCCCCAAITCAGCGGGAAGCAGIIAAGAGCGGI
                                                                                                                                                                                                                                                                         CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGT-TGAGAGGGGGGACTGAGAGA
                                                                                                                                                                                                                                                                                                                                  300 CAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
                                                  Gaps
                                                  15;
                    Length 771;
                                                  Indels
                        DB 4;
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Pred. No. 2.1e-129
0; Mismatches 49;
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CR625046.1 GI:50505853
HTC; CNSLT_CDNA.
HOMO sapiens (human)
Homo sapiens
                          76.5%;
89.9%;
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/mol_type="mRNA"
/db_xref="taxon:99806"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                    2452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIO87886 771 bp mRNA linear EST 20-JUN-2001
602852690FI NIH_MGC_10 Homo sapiens CDNA clone INAGE:4993894 5',
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1 (hases 1 to 771)
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                         421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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   CTGGACCGGCCTGCTAGCCCCATGCTCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                    2093 GAAATCTCAGCTGCACAACCTCTACTACGCCCCAATTCAGCAGAAGCAGTTAGAGCGGT
                                                                                                                   CATCAGCCAACTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGGACTGAGAGA
                                                            GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can http://image.llh.gov
http://image.llh.gov
Plate: LiAMI1015 row: d column: 23
High quality sequence stop: 762.
                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BI087886
BI087886.1 GI:14506216
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Homo sapiens
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BI087886
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/organism="Homo sapiens"

mol_type="mRNA"

/mol_type="mRNA"

/db_xref="texcn:9606"

/tissue_type=="mbryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"

/clone_lib="GRN PRENEU"

/note="foligo dT primed, full-length enriched cDNA library fnote="foligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427 TICCIAGGCTGACTAAGAATCCCTAAGCCTAGCTGGAAGGTGACCACATCCACCTTTAA 486
                                            Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human Es cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 AATGGAGCCCAAGATGCAGTCCAAGACTAAGATCTACGCAGACCCCTGGACCTGGCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 AATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCCCTGGACCGGCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 TAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAATCTCAACTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 ACAACCCCTACTATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGTCATCAGCCAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 ACAACCTCTACTACGCCCCAATTCAGCAGGAAGCAGTTAGAGCGGTCGTCGGCCAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGACTGAGAGACAGGACTAGCTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 719;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 719)
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                                                                                                                                                                                                                                                                 94025,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.1%; Score 470.6; DB 7; 92.7%; Pred. No. 4.7e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                      Geron Corporation
230 Constitution Drive, Menlo Park, CA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 719 Std Brror: 0.00.
Location/Qualifiers
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                                                                                                                                                                                                                  Regenerative Medicine
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Best Local Similarity 92.7
Matches 494; Conservative
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BX365066/c
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AUTHORS
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COMMENT
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr - www.genoscope.cns.fr at www.genoscope.cns.fr at strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2646 AGAGCACAGCAGGAGGACAATGATCGGGATATAAACCCCAAGTCTTCGAGCCGGCAACGG 2705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            719 bp mRNA linear EST 16-MAY-2004
Ното варієпя cDNA 5', mRNA sequence.
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCTTAGCTGGGAAGGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2526 ACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTGACCAATCAGAGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2586 ACTAAAATGCTAATTAGGCAAAGACAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                76.4%; Score 485; DB 3; I
llarity 91.1%; Pred. No. 4.1e-129;
Conservative 0; Mismatches 40;
                                                                                                                                                                                                                1. 2748
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs0D1044YK06"
/plasme_rype="Placents Cot 2:/plasmid="pcMVSPORT_6"
                                                                                                                                                                                            Location/Qualifiers
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Matches 531; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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COT 25-NORMALIZED Homo sapiens CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db xref="taxon:9606"
/clone="CSD102212113#
/tissue type="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
480
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                                   163 ACTAAAATGCTAATTAGGCAAAGACAGGAGGTAAAGAAATAGCCAATCATTGCCTG
                                                                             481 AGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                      103 AGAGCACAGCAGGAGGACAATGATCGGGATATAAACCCAAGTCTTCGAGCCGGCAACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 758;
                                                                                                                                                            CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTT 584
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                                                                                                                                                                                 CAACCCCTTTGGTNCCCTCC-TTGTATGCGASMTCKGTTTT
                                                                                                                                                                                                                                                                                                    BX357208 Momo sapiens PLACENTA COT 25-NORM clone CS0DI022YJ18 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 466.6; DB 5;
Pred. No. 6.8e-124;
9; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For more information about this cluster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                   BX357208.2 GI:46305595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.5%;
illarity 88.8%;
Conservative 9
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Best Local Similarity
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BX357208/c
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VERSION
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BP 191 91006 EVRY cedax - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSDNT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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        EST 08-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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        O MRNA linear EST 08-APR-200 COT 25-NORMALIZED Homo sapiens CDNA
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                                                                                                                                                                                                                                                                                     On May 5, 2003 this sequence version replaced gi:30374869.
Contact: Genoscope
                                                                                                                                                                                         Catarrhini; Hominidae; Homo
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                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                        1 (bases 1 to 1071)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
          BX365066 1071 bp mRNA BX365066 Homo sapiens PLACENTA COT 25-NORW CLONE CSODIO46YA18 3-PRIME, mRNA sequence-BX365066
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      1071 bp
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/db_xref="taxon:9606"
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                                                                                            AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 360
                                                                                                                   AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACC 229
                                                                                                                                                                                                                                                   AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG 540
                                                                                                                                                                                                                                                                  AGAGCACAGCAGGAGGGACACATGATCGGGATATAAACCCCMMSYCCCCGCGCCGGGCCACGG 49
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (basea I to 2716)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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full-length cDNA clone CS0DE013X120 of Placenta of Homo sapiens
                                                       CGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGGACTGAGAGACC
                GAAATCTCAGCTGCACAACCTCTACTACGCCCCAATTCAGCAGGAAGCAGTTAGAGCGGT
                                       CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
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Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Pred. No. 3.4e-123;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                       CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGG 573
                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DE013Y120"
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/plasmid="pCMVSPORT_6"
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HTC; CNSLT_CDNA.
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Homo sapiens
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Homo sapiens (Induction)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dases I to 998)

Si i,W.B., Gruber,C., Jessee,J. and Polayes,D.

Rull-length cDNA libraries and normalization

M. On May 2, 2003 this sequence version replaced gi:30337641.

Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage

Bp 191 91006 ENRY cedax - France

Email: seqref@genoscope.cns.fr www.genoscope.cns.fr

ist sirand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Econ V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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2168 CCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCTTCCAGAATCGAAGCTGTAAAAACTA 2227
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83337769 Homo sapiens FLACENTA COT 25-NORWALIZED Homo sapiens CDNA
Clone CSODIO51YM13 3-PRIME, mRNA sequence.
BX337769
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                                                                                                                                                                                                                                         CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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/mol_type="mRNA"
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Deficiency Control Marchan of Control of Con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
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                                                                                                                                                                                                                                                                                      For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI018CD04NP1&c=4215.r. Location/Qualifiers
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ilarity 87.0%; Pred. No. 4.3e-120;
Conservative 1; Mismatches 63;
- Centre National de Sequencage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCT 479
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Pull-length cDNA libraries and normalization Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30439129. Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAA-GGCACCCCTCCCGA 179
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                                   /clone="CSODIO51YM13"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                            Score 454.2; DB 5;
Pred. No. 2.9e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                        xref="taxon:9606"
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89.1%;
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Homo sapiens
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BX378303/c
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/lange/image.html
Insert Length: 1645 Std Error: 0.000
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/clone lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and clonned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 31-DEC-1998
                                                                                                    246 AAGAGGGCTCACTAAAATGCTAATTAGGCAAAAAACAGGAGGTAAAGAAATAGCCAATAAT 187
                                                                                                                                                                                                     471 CTATTGCCTGAGAGCACAGGGGGAGGGACAAGGATGGGGATATAAACCCCAGGCATTCGAG 530
                                                                                                                                                                                                                                                186 TTATTGCCTGAGAGTACAGCGGGAAGGACAATGATCGGGATATAAACTCATGCATTCGAG 127
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 494)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA781423 494 bp mRNA linear EST 31-DEC-3aj26c03.sl Soares_testis_NHT Homo sapiens cDNA clone 1391428 3' similar to contains PTR7.tl PTR7 repetitive element ;, mRNA
                                                  -AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                     531 CCGCCAACGCCAACCCCCTTTGGGTCCCCTCCCTTTGTATGGG 573
                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                           126 CCACCAATGGCTACCCTCTTTGGGTCCCCTCCCTTTGTTATGG
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High quality sequence stop: 475.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1391428"
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AA781423/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-AUG-2001) Asao Pujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
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Pan troglodytes DNA, clone: PTB-130M15.F, genomic survey sequence.
AG121669
AG121669.1 GI:16650834
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                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                             Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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llarity 88.3%; Pred. No. 2.6e-119;
Conservative 0; Mismatches 58;

    689
    organism="Pan troglodytes"

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/db_xref="taxon:9598"
/clone="PTB-130M15.F"
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                                                                                                                                                           Pan troglodytes (chimpanzee)
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R.Site 1 : SacI
R.Site 2 : SacI.
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EST383642 MAGE resequences, MAGL Homo sapiens CDNA, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
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                                                                                          Length 1019;
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                                                                                                                              66; Indels
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68.5%; Score 435; DB 5; I
Best Local Similarity 83.4%; Pred. No. 1.1e-114;
Matches 494; Conservative 19; Mismatches 66;
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BP 191 91006 ENRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dI) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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Li (bases 1 to 1019)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Pull-length cDNA libraries and normalization
Onpublished (2001)
On May 15, 2003 this sequence version replaced gi:30771765.
Contact: Genoscope
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/tissue type="PLACENTA"
/clone=lib="Homo sapiens PLACENTA"
/note="Vector: pCMYSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
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                                  CTGCACACACCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGTCATCAGCCAA
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE012DE12NP1&c=4215.r.
Location/Qualifiers
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/db_xref="taxon:9606"
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/note="Organ: spleen; Vector: Uni-ZAP XR; Site 1: EcoR I; Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit (Catalog #200450)"
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      WA 98134,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="mononuclear lymphocyte"
/dev_stage="adult"
/lab_host="B. coli SOLR"
/clone_lib="Katze_MMSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.7%; Score 430.2; DB 7;
83.8%; Pred. No. 2.5e-113;
iive 0; Mismatches 88;
      Suite 450, Seattle,
2203 Airport Way S, Suite 450, Seattle, Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.02.24. 676 Q20 bases.PCR PRIMERS
FORWARD: CCCTCACTAAAGGGAACTAGGTA
BACKWARD: CCCTCACTAAAGGGGAATTGGGTA
INSET Length: 870 Std Brror: 0.00
Plate: CL000135 row: H column: 02
Seq primer: CCCTCACTAAAGGGGAACAAAA
POLYA=NO.
                                                                                                                              равев
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9544"
/clone="IBIUW:10227"
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 83.8
Matches 527; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
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ILLUWIGEN MCQ 23968 Katze MMSP Macaca mulatta cDNA clone
Unigene Hs.349001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343
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(a. Cases I to 870)

Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L. Large-scale Rhesus Macaque cDNA Sequencing

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 AACCCAGGCATTCGAGCCAGCAACCGCCATTGGGTCCCTTTCCCTTTGTATGGGA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 GTTCAGCAGGAAGCAGTTAGAGTGGTCATCAGCCAACCTCACCAACAGCACTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTAAGCCTGGGAAGGTGACTGCATCCACCTCTAAACATGGGGGCTTGCAACTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 ATGACTAAGATCCACCGTGGACCCCT-GGACCGGCCTGCTAGCCCCATGCTCCGATGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGACATTGAAGGCACCCCTCCCGAGGAAA-TCTCAACTGCACAACCCCTACTATGCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                            68.1%; Score 432.4; DB 2; Length 522; 91.8%; Pred. No. 5.2e-114; Indels 2:ive 0; Mismatches 41; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             575 GCTCTGTTTTCACTCTATTTCACTCTATTAAATCTTGCAACT 616
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                                                                                                                                                        /organism="Homo mapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone lib="MAGE resequences, MAGL"
/note="Vector: pBluescriptSKm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta (rhesus monkey)
Macaca mulatta
                                                             Seq primer: Forward.
Location/Qualifiers
1. .522
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Illumigen Biosciences Inc.
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   Email: johnq@tigr.org
Plate: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 479; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342
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AUTHORS
TITLE
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COMMENT
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CN645411
                                                                                                 FEATURES
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320

465 380 525 431 582 489 645

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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (102-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:sia 1-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                            .089 CGACGGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGTACTGAGAGAGC 1148
                                                                                                                                                                       1209 rieciacciarizaraciacada actrificaria de carcacacare de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente de construirente 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AG033781 653 bp DNA linear GSS 01-NOV-2001
Pan troglodytes DNA, clone: PTB-008021.F, genomic survey sequence.
AG033781
                                                                                                                                                                                                                                                                                                                                                                                              467
                                                                                                                              AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCT-GGGAAGGTGAC 359
                                                                                                                                                                                                                                                      360 IGGATCCACCICTAAACATGGGGC--TTGCAACTTAGCTCACACCCGACCAATC---- 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526
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CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 300
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                              412 ---AGAGAGCTCACTAAAATGCTAATTAGGC-AAAAATAGGAGGTAAAGAAATAGCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 CATCTATTGCCTGAGAGCACAGGGAGGGACAAGGATCGGGATATAAA-CCCAGGCATT
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .653
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Pan troglodytes
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          241
                                                                                                                                            301
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AG033781/c
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This clone has the following problem: retained intron.
Location/Qualifiers
1. .1500
/organism="Homo Sapiens"
/mol type="Homo Sapiens"
/mol type="Homo Sapiens"
/mol type="mRNA"
/db_xref="mRNA"
/db_xref="mRNA"
/clone="IMAGE1770655"
/tissue type="Placenta"
/clone=IMAGE1770655"
/tissue type="Placenta"
/clone=Imbe="NHTM MGC 79"
//ab host="MHTM MGC 79"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.AG.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               969 cresaccasccrecrascccarscrecsarsrraarsacarcsaasscrecrecresss 1028
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                                                                                                                                                                                                                                                                              HTC 04-MAR-2003
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (02-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTGTAAAACTA
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                                                                                                                                                                                                                                                                              linear
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Contact: MGC help desk
Email: progbs-remail.nih.gov
Finsle: procurement: CLONTECH
                                               635
                                                                                                      766 GCTCAAAAAAAAATATTAAAAAAAAAA 794
                                                                                                                                                                                                                                                                1500 bp
Homo sapiens, clone IMAGE:4770655,
BC026287
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                                               607 TCTTGCAACTGAAAAAAAAAAAAAAA
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1500)
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Homo sapiens
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Matches 557; Conservative
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                                                                                                                                                                                                             RESULT 18
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Clone distribution: NCI-CGAP clone distribution information found through the I.M.G.B. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/liange/image.thml
Insert Length: 1407 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 455
POLYAR-NO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.5%; Score 415.8; DB 1; larity 92.9%; Pred. No. 3.4e-109; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                         1. .490
/organism="Homo sapiens"
                                                                                                                                                                                                         Location/Qualifiers
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BE732673
BE732673.1 GI:101466
BST.
Homo sapiens (human)
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Matches 435, Conserv
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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NCI/MINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological bisorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP); Tumor Gene Index
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                                                                                          Gaps
                                                                                          18;
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                                Score 423; DB 9; Length 653
Pred. No. 2.9e-111;
0; Mismatches 52; Indels
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                                   66.6%;
88.0%;
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                                   Query Match
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cDNA clone IMAGE:5670930 3', mRNA sequence.
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BI963185.1 GI:16337590
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Best Local Similarity 88.33
Matches 467; Conservative
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Fax: 617-495-8557
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RESULT 22
BI963185/c
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                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 440)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCW752 row: j column: 01
High quality sequence stop: 440.
Location/Qualifiers
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                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTATTAAATCTTGCAACTG 617
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Best Local Similarity 94.1
Matches 413; Conservative
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AUTHORS
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COMMENT
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/clone ъ, 484 B1963185 543 bp mRNA linear EST 12-MAR-2002 Email: dmaltonoblohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Mashington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stop: 451. 134 CTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAATCTCAACTG 193 Eukaryotza, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 543)

1 (bases 1 to 543)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Bape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Williams, T., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Bndocrine Panceas Consortium

Unpublished (2000) Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, 74 AAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCCCTGGACCGGCCTG 51; Indels 11; Gaps 62.4%; Score 396; DB 4; Length 543; 88.3%; Pred. No. 1.9e-103; ive 0; Mismatches 51; Indels 1

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To (bases I to 651)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (652);
1-7-22 Suchiro-chou, Tsuruni-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clonnes are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 02-NOV-2001
                                                                                                                                        CCCTGTATCTTTAACCTCCTTGTTAACTTTTGTCTTTCCAGAATCGAAGCTGTAAAACTA 515
                                                                                                                                                                                       CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC 120
                                                                                                                                                                                                                                                                                   CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG 180
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Pan troglodytes DNA, clone: PTB-046A08.R, genomic survey sequence.
AGOS8970
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Length 966;
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Score 395.2; DB 5
Pred. No. 3.7e-103
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                                              22; Mismatches
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  62.2%;
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                        Similarity
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Query Match
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX380176 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA CLONE CSODIO44YKO6 3-PRIME, mRNA sequence.
BX380176.2 GI:46834414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CSODIO44YK06"
/tissue type="PLACENTA COT 25-NORWALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="Ist strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                      365
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                                                                                                                                                                                                                                                                                                                                                                                                      484
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                              CCCCAACAGCACTTGGGTTTT-CTGTTGAGATGGGGGACTGAGAGAGAGACAGGACTAGCTGGA
                                                                                                                                                                                                                                            CCCCAACAGCACTTGGGTTTTCCTGTTGAGGGGGGGACTGAGAGACAGGACTAGCTGGA
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                        CACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGTCATCAGCCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI044BF03NP1&c=4215.r.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 966)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
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AUTHORS
TITLE
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ACCESSION

COMMENT

FEATURES

DRIGIN

RESULT 23

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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (102-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
T-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:sis 18-145-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAACCCCCT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 CAGGAGGACAATGATGAGGATATAAACCCAGGCATTCGAGCCAGCAACAGCTACCCTCT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAGGCTGACTAAGAATCCCTAAGACTAGCTGGGAAGGTGACCACATCCACTTGAAACA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 CCATGCTCCGATGTTAATGACATTGAAGGCACCCCT-CCCGAGGAAATCTCAACTGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 GAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCCCTGGACCGGCCTGCTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               651 GACCCCGAGATCCAGTCCATGACTAAAGACTACTGTGAACCCCTGGACTGGCCTGCTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                // sex="male"
// cell type="lymphoblast"
// clone lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCAC
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            Taylor, T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.9%; Score 393.2; DB 9;
88.1%; Pred. No. 1.3e-102;
ive 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                               1. .701
/organism="pan troglodytes"
/mol_type="genomic DNA"
/db &ref="taxon:9598"
/clone="PTB-137E19.F"
          Fuijyama, A., Hattori, M., Toyoda, A.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                           Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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Pan troglodytes DNA, clone: PTB-137E19.F, genomic survey sequence.
AG126669
                                                                                                                                                                                                                                                                                                                                                                                    554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCATGCTCCGATGTTAATGACATTGAAGGCACCCTCCCGAGGAAATCTCAACTGCACA 197
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Pan troglodytes
Eukaryotas Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                      651;
                                                                                                                                                                                                   /eex="male"
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                                                                                                                                                                                                                                                                                   Score 394.8; DB 9; Length
Pred. No. 4.4e-103;
0; Mismatches 57; Indels
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                                                                                                   Location/Qualifiers
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                    Sequencing: M13Rev
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nilarity 87.6%; E
Conservative 0;
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R.Site 2
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                                                       Vector
     PRIMERS
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AG126669/c
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Insert Length: 1375 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA837267 443 bp mRNA linear EST 31-MAR-1998 od26b10.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1369051 similar to contains PTR7.t1 PTR7 repetitive element ;, mRNA
                                                                                                                                                                                                                                          307 ACCTGGGAAGGTGACCACTTCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACATG 248
                                                                                                                                                                                           127 ACCCAGGCATTTGAGCCAGCAATGGCAACCCCCTTTGGGTCCCCTTTGTATGGGAG 68
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 443)
NCI-(GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                    247 ACCAATCAGATAGTAAGGAGGCTCACTAAAATGCTAATTAGGCAACAACAGGGGGTAAA
                                                                                                                                                                                                                                                                                                                    516 ACCCAGACATTCGAGCCGGCAACGCCAACCCCTTTGGGTCCCCTTTGTATGGGCG
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                   405 ACCAATCA-----GAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (SSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:s1-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanizee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                           GSS 03-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 AGCCCTTCTCCCCAAGGAAATCTCAACTGCACCACCCCTACTACACACCCCAATTCAGCAGG 427
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                                                                                                    AG066901
Pan troglodytes DNA, clone: PTB-056L15.F, genomic survey sequence.
AG066901
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                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.9%; Score 393; DB 9; Length 609; 87.7%; Pred. No. 1.4e-102; ive 0; Mismatches 55; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-056L15.F"
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R.Site 2 : SacI.
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Best Local Similarity 87.7%;
Matches 478; Conservative
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qc61h10.xl Soares placenta 8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1714147 3' similar to contains PTR7.bl PTR5 repetitive element; ' mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGG 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 TGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAAT----
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                                                                                                                                                                                                                                                          56 AACTACAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTG
                                                                                                                                                                                                                                                                                                                          116 GACCCCTGGACCGGCCTGCTAGCCCCATGCTCGATGTTAATGACATTGAAGGCACCCTC
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                                                                                                /clone lib="CIT Approved Human Genomic Sperm Library /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones i E-Coli DH108"
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                                                                                                                                                                                             DB 8;
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                                                                                                                                                                                        tch al Similarity 82.2%; Pred. No. 7.2e-101; 484; Conservative 0; Mismatches 94;
                                            /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="plate=3131 Col=8 Row=J"
                             organism="Homo sapiens"
Location/Qualifiers
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Homo sapiens
                                                                                              'sex="male"
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HS 3131 B2 E04 MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3131 Col=8 Row=J, genomic survey
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                                                                                                    CAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGACAGG 303
                                                                                                                                                                         CAGCCAACCTCACCAACAGCACTTGGGTTTTCCTGTTGAGAGAGGGGACTGAGAGAACAGG 324
                                                                                                                                                                                                                  ACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACTGCA 363
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Bukaryota;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 712)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. ar
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                                                                                 184 ATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGTCAT
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
                                                  1;
                 Length 443;
                                                  25; Indels
               Score 392.6; DB 1;
Pred. No. 1.8e-102;
0; Mismatches 25;
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High quality sequence stop: 712
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AQ892947.1 GI:6349137
                 Query Match 61.8%;
Best Local Similarity 94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 TTAGGTTTTCCTGTTGAGATGGGGGACTGAAAGACAGGACTAGCTGGATTTCCTAGGCTG 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the INAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 720 StG Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 428.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACCACCTCTTTAAACACGGGGCTT
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0; Mismatches 27;
                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                      Contact: Robert Strausberg, Ph.D.
           Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                 Matches 403; Conservative
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EST 30-MAR-1999

446 bp mRNA linear ES: tg45g04.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2111766 3', mRNÄ sequence.

AI393478

ACCESSION

LOCUS DEFINITION AI393478/c

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                                                                                                                                                                                                                                                                                       (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1061 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 445.
Location/Qualifiers
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                                            Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 446)
                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
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Homo sapiens (human)
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Unpublished (1997)
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36 TAAATCTTGCAACTGCAAAAAAAAAAAAAA 4

Search completed: January 22, 2005, 19:31:32 Job time : 1902.54 secs

Sequence:

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Minimum Maximum M

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Tobases 1 to 1481)
Perron, H., Beseme, F., Bedin, F., Paranhos-Baccala, G.,
Komurian-Pradel, F., Jolivet-Reynaud, C. and Mandrand, B.
Isolated nucleotide sequences associated with multiple sclerosis or
rheumatoid arthritis and a process of detecting
Patent: US 6582703-A 105 24-JUN-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ACGCGCCTTCCTGGAAATATTGATGCCCCATCATAGGGGTTTATCTAAGGGAAACTCC 180
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; Pred. No. 0;
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AR344387
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AF506835
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BD232464
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AL330039 Human DNA
CQ713381 Sequence
BD525040 Method fo
AX036992 Sequence
AF331500 Multiple
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Pan trogl
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Hylobates
                                                        ; Search time 6212.46 Seconds (without alignments) 11273.477 Million cell updates/sec
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BD136197 Retrovira
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AX101580 S
AC101586 P
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AUTHORS Baccala,G.P., Pradel,F.K., Bedin,F., Sodoyer,M., Ott,C., Mallet,F.,
Perron,H. and Mandrand,B.

TITLE Retroviral nucleic material and nucleotide fragments, in particular, associated with multiple sclerosis and/or rheumatoid arthritis, for diagnostic, prophylactic and therapeutic uses arthritis, for diagnostic, prophylactic and therapeutic uses blo MERIEUX

GS Unidentified by 2002509437-A/7

PD 26-MAR-2002;
PP 07-JUL-1998 JP 100-7

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BERNARD MANDRAND
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Strandedness: Single;
Topology: Linear;
Retroviral nucleic material and nucleotide
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CC associated with multiple sclerosis and/or rheumatoid arthritis,
CC diagnoration
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GGAGCCACTGTCTGTTGGTTTACTTCACCCATACCAGTATGTCTGATGGGGGTGGAATT 360

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PAT 18-SEP-2002

BD136197 18-SEP-20 Retroviral nucleic material and nucleotide fragments, in particular, associated with multiple sclerosis and/or rheumatoid

RESULT 3 BD136197 LOCUS DEFINITION

CAAGGTCAGGCAAGAGAAAACAAGTAAAGGAAGCAATCTCCCAACTGACCGGGGACAT

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Komurian-Pradel, F., Paranhos-Baccala, G., Bedin, F.,
Komurian-Pradel, F., Paranhos-Baccala, G., Rajoharison, A., Garcia, E.,
Munanian-Paraz, A., Sodoyer, M., Ott, C., Rajoharison, A., Garcia, E.,
Mallet, F., Mandrand, B. and Perron, H.
Direct Submission
Submitted (10-FBB-1999) UMR103 CNRS, bioMerieux, 46, allee
D'Italie, Lyon 69007, France
Location/Qualifiers
                                                                                                             Multiple sclerosis associated retrovirus element
Multiple sclerosis associated retrovirus element
Viruses; Retroid viruses; Retroviridae.

1 (bases 1 to 1932)
Komunian-Pradel,F., Paranhos-Baccala,G., Bedin,F.,
Munnian-Pradel,F., Sadoyer,M., Ott,C., Rajoharison,A., Garcia,E.,
Mallet,F., Mandrand,B. and Perron,H.
Molecular cloning and characterization of MSRV-related sequences
associated with retrovirus-like particles
Virology 260 (1), 1-9 (1999)
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    1932
/organism="Multiple sclerosis associated retrovirus
element"

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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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/db_xref="taxon:89382"
/clone="CL15"
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AF127228.1 GI:5726293
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                                          CAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCAGGCCATACATTCAATC
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                                                                            CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC
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Direct Submission

Submitted (19-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, Ciallo 1834, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Sep 19, 2000 this sequence version replaced gi:9944073.

During sequence assembly data is comparated from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may note be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSEROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence in contings of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX

IMPORTANT This sequence is not the entire insert of clone RR13-383K5 It may be shorter because we sequence overlapp. The true left end of clone RP13-383K5 is at 1 in this sequence. The true left end of clone RP13-383K5 is at 1 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known ambiguous, there is an annotation using the 'unsure' feature key.

RP13-383K5 is from the library RC1-13.2 constructed by the group of Pieter de Jong, For further details see
                                                                                                                             AL390039

Human DNA sequence from clone RP13-383K5 on chromosome Xq22.1-24
Contains ESTs, STSs and GSSs. Contains a novel gene and a novel
Gene similar to NUP62 (nucleoporin 62kD), complete sequence.
AL390039
                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 162579)

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/clone="R$13.388.5"
/clone="Ib="RPCI-13.2"
/clone=lib="RPCI-13.2"
/note="match: GSS: Em:AQ036363"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic_DN
/db_xref="taxon:9606"
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/note="match: GSS:
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                                                                                                       AGCACCCCTAGCCCCTACAAAGGACTACTCTCTCAAAACTACATGAAACCTCCGTACC 480
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                                           CAAGGTCAGGCAAGAGAAAAAAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACT
                                                                                                                                                                                                                                                                       CAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCAGGCCATACATTTCAATC
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                     CAAGGTCAGGCAAGAAAAAAAGTAAAGGAAGCAATCTCCCCAACTGACCCGGGGACAT
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e="match: GSS: Em:AQ054794 Em:AQ823559"

repeat_region 11	11431456 /nore="Alusx repeat: matches 1312 of consensus"	/note misc_feature 16067
repeat_region 14	repeat: matches 356	note repeat_region 16923
repeat_region 29	9223739 note="LIPA2 repeat: matches 53296146 of consensus"	repeat_region 17107
m \	8444087 note="L1M4 repeat: matches 1251 of consensus"	repeat_region 17175
	40924231 /note="L1M4 repeat: matches 612756 of consensus"	repeat_region 17839
repeat_region 43	43734559 /note="LIM4c repeat: matches 9711152 of consensus"	repeat_region 18213
repeat_region 45	45864619 /note="17 copies 2 mer aa 100% conserved"	repeat_region 18706
repeat_region 46	5234964 hote="MLT1A1 repeat: matches 3333 of consensus"	repeat_region 18812
	49895149 /note="L1MA8 repeat: matches 61206288 of consensus"	repeat_region 19058
	51525602 /note="L1PA15 repeat: matches 53255779 of consensus"	misc_feature compl
repeat_region 56	606, .5916 note="AluSq repeat: matches 1313 of consensus"	repeat_region 19556
20 ~	9176014 note="49 copies 2 mer ga 75% conserved"	repeat_region 19873
9 ~	0186409 note="LIPA15 repeat: matches 57696157 of consensus"	repeat_region 21587
9 ~	5666750 note="L1M4 repeat: matches 28573036 of consensus"	repeat_region 22298
repeat_region 67	7517063 note="AluJo repeat: matches 1307 of consensus"	repeat_region 22743
r \	0648097 note="LIM4 repeat: matches 30364105 of consensus"	repeat_region 23049
repeat_region 80	0998419 . note="AluSx repeat: matches 1306 of consensus"	repeat_region 23285
repeat_region 84	4208487 note="LIMC/D repeat: matches 55825648 of consensus"	repeat_region 23364
repeat_region 10	003910396 note="THE1B repeat: matches 1364 of consensus"	repeat_region 23425
repeat_region 1		repeat_region 24306
repeat_region 1		repeat_region 24594
repeat_region 1	144811983 note="L1MD3 repeat: matches 71627739 of consensus"	repeat_region 25110
repeat_region 1	203012337 note="AluSx repeat: matches 1309 of consensus"	repeat_region 2543
repeat_region 1	299513077 note="MIR repeat: matches 103186 of consensus"	repeat_region 2577
repeat_region 1	311013222 note="FLAM C repeat: matches 2124 of consensus"	repeat_region 2596
repeat_region 1	1322813518	repeat_region 2613:
repeat_region 1	351913853 note="MER7A repeat: matches 1346 of consensus"	repeat_region 2655/
repeat_region 1	385414039 note="LIMEc repeat: matches 19512131 of consensus"	repeat_region 2671.
repeat_region 1	404014254 note="MER20 repeat: matches 1218 of consensus"	repeat_region 2698:
	425514807 note="L1MEc repeat: matches 16861951 of consensus"	repeat_region 2718:
region	1480815105 /note="Aluab repeat: matches 1311 of consensus"	
	51061547. note="LimEc repeat: matches 13091686 of consensus" 1603	Best Local Similarity Matches 1473; Conserva
ropeat_region /	incre="Lines repeat: matches 58236167 of consensus" 7824 15620	Dy 1 Arggcccrccc
. ~ ~	repeat: matches	Db 21559 ATGGCCTCCC
_		Qy 61 GCACCCCTCC
	/note="match: GSS: Em:AQ769824" complement(15927, .16073)	Db 21499 GCACCCCTCC

18213. .18318
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49. .23286
49. .23286
50. .23361
62. .23361
62. .23361 'LIMBS repeat: matches 5623. .6135 of consensus" .23048 CITAICAIACITITCICITITACIGITCICITACCCCCTITCGCICTCACI 82. .27307 te="Lip4 repeat: matches 5454. .5584 of consensus" 10. .25436 -e="LiM3 repeat: matches 5101, .5440 of consensus" 13-.25742 18-.13594 repeat: matches 1. .307 of consensus" 19. .25961 repeat: matches 4019. .4084 of consensus" e="L2 repeat: matches 1244. .1898 of consensus" 9. .18106 e="MER70A repeat: matches 148. .418 of consensus" 0; Gaps 64. 23429 te="1.1M4 repeat: matches 4019. .4084 of consensus te="1.1 repeat: matches 3097. .4043 of consensus" te="1.1 repeat: matches 1. .293 of consensus" te="MluJo repeat: matches 1. .293 of consensus" 94. .25109 te="1.1 repeat: matches 2600. .3097 of consensus" 3. 16998 e="18 copies 2 mer at 71% conserved" 7. 1716 e="12 repeat: matches 2688. 2750 of consensus" 5. 17755 99.1%; Score 1468.2; DB 9; Length 162579; 99.5%; Pred. No. 0; ive 0; Mismatches 8; Indels 0; Ga e="mix.repeat: matches 1. .89 of consensus" 15. .26328 7. .16294 e="match: GSS: Em:AQ457003"

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1201 GGAGAAGAACGCTGTTATTGTTAATCCAGAATTGTCACTGAGAAAGTTAAGAA 1260	RESULT 6 CQ719381 LOCUS CQ719381 LOCUS DEFINITION Sequence 5315 from Patent W002068579. ACCESSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION VERSION MAMMala. Homo sapiens CQ719381. GQ719381. GQ719381. GG719381 GG719381. GG719381 GG7193	JOURNAL Patent: WO 02068579-A 5315 06-SEP-2002; PEATURES Location (NY) (US) FEATURES Local Similarity 99.4%; Pred. No. 0; Matches 1472; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	ATGGCCTCCCTTATCATACTTTCCTTTACTCTTACCCCCTTTCGCTCTCACT 60	216 ACCTTCACTGCCCCACACCCCGCACTGCTATAACTCTGCCCCTTTGCATG 275 Qy 241 CATGCAAATACTCATTATGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT 300
121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC 180 21439 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATAGGAGTTTATCTAAGGGAAACTCC 21380 ACGCGGGTTCCTGGAAATATTGATGCCCGCAACTGCTATATTTTTTTT	421 AGCACCCCTAGCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCTCCGTACC 480 21139 AGCACCCCTAGCACAAGGACTAGTTCTCTCAAAACTACATGAAACCTCCGTACC 21080 481 CATACTCGCCTGGTGAGCCTATTTAATACCACCTCGGCTCCATGAGGTCTCAGCC 540 [GGACCTCTTGTTTCCAATCTGGAATAACCCATACCTCAACCTCACCTGTGTAAATTT [20719 AATGGCTCTTCAGAATCTATGTCTTCTTTTTTTTTTTTT	GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTCCTTAGCAGCAGTAGTCCTT GTCAAAATCGAAGAGCTTTAGCAACAGCACGCCAAAAGAGGGGGAACCTGTTAATTTTA CAAAATCGAAGAGCTTTAGACTTGCTAACGCCCAAAAGAGGGGGAACCTGTTTATTTTA CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA

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15. CANGEL/GECOMAGGAMACANTENAGAMACHATECCAA/CECCACGAGGACAT 455 15. CANGEL/GECOMAGGAMACHATECCAA/CECCACGAGGACAT 455 15. CANGEL/GECOMAGGAMACHATECCAA/CECCACACGAGGACAT 455 15. CANGEL/GECOMAGGAMACHATECCAA/CECCACGAGGACAT 455 15. CANGEL/GECCACGAGGACAA/CECCACGAGGACAA/CECCACGAGGACAA/CECCACGAGGACAA/CECCACGAGGACAA/CECCACGAGGACAA/CECCACGAGGACAA/CECCACGAGGACAA/CECCACGAGGACAA/CECCACGAGGACAA/CECCACGAGGAA/CECCACACGAGGAA/CECCACACGAGGAA/CECCACACGAGGAA/CECCACACGAGGAA/CECCACACCACA	141 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAAG 	RESULT 7 BD252040 BD252040 BD252040 DEFINITION Method for detecting superantigen activ ACCESSION BD252040 VERSION BD252040.1 GI:33061810	Homo sap Homo sap Eukaryot Mammalia	AUTHORS PETCON, H. and Lafont, M. TITLE Method for detecting superantigen activ JOURNAL Patent: JP 2002539804-A 1 26-NOV-2002;	COMMENT OS Homo sapiens (human) PN JP 2002539804-A/1 PD 26-NOV-2002 PP 20-MAR-2000 JP 2000607009	ΥE	PC C07K14/47,C07K16/18,C12N7/00,C12Q G01N33/15, PC G01N33/50.G01N33/569.G01N33/577//C12P2	(CI2Q1/02,CI2R1:93), (CI2Q1/68,CI2R1:9: A61K37/02 CC Method for detecting superantigen sammle	FH Key Location/Qualifie FT source 11629 FT Source /organism='Homo s	rce	98.7%; SCC	U 7=	1 ATGGCCTCCCTTATCATACTTTTCTCTTTACTGTT 61 GCACCCCTCCATGCTGCTGTACAACCAGTAGCTCC	61 GCACCCCTCCATGCTGCTGTACAACCAGTAGCTCC		181 ACCTTCACTGCCCACACCCATATGCCCCGCAACTGC	241 CATGCAAATACTCATTATTGGACAGGGAAAATGATT	301
151 CAMOGTICAGGOANGAGAMANAGANGCANTICTCCCAACTGACCCCGGGACAT 152 ACAGCTCCACCTACAACAAAAAAAAAAAAAAAAAAAAAA	yo da	RES BD2 DD2 ACC	SOU	RE CLI	CO				7 23	i	OR	ď	qa Yo	1 A &	S A	Sy Sp	δ f	8 8
	CAAGGTCAGGCAAGAAAAAAAAGTAAAGGAAGCAATCTCCCAACTGACCGGGGACAT 	AGCACCCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCTCCGTACC 48	CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC CAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCAGGCCATACATTTCAATC	CCIGITCCTGAACAATGGAACAACTICAGCACAGAATAAACACCACTICCGTITIAGTA 	GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT 	AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACACGA 78	ATAGICIGCCIACCCICAGGAAIAITITIGICIGGGAACCCICAGCCIAICAITGITIG 	AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC	actgaacaagatttatacaatcatgtcgtacctaagccccacaacaaagagtaccatt 	CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGCAGCACTGGCAGTATC	acaactttactcagttctactacaaactattctcaagaaataaat	GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT	CABARTCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA	GGAGAAGAAGCGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA	GGAGAAGATIGTTATTATGTTAATCAATCCAGAATTGTCATGAAAATGTCAGAGAATGTCAGAAAAAAAA		CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG	TTACTCCTCTTTGGACCCTGTATACTTTACACTCCTTTAGTTTAGTTTGCTTCCTAGTTTTTTTAGTTTTGTTTCTTCCAGAATTTTACCTCCTTCCT

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                                                                                                                                                                                                                                                                                                                                     Q1/02, C12Q1/68, G01N27/447, PC
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(93),C12N15/00,G01N27/26, PC
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hini; Hominidae; Homo.
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Catarrhini, Hominidae, Homo.
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Patent: FR 2791140-A 1 22-SEP-2000;
BIO MERIEUX (FR)
Location/Qualifiers
1. 1629
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/db_xref="taxon:9606"
                                                                                                            DNA
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                                                                                                         AX036992 1629 bp
Sequence 1 from Patent FR2791140.
AX036992 GI:11226420
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
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independent from the T-cell receptor antigen specificity"
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Camelo,S., Dumon,A., Jolivet-Reynaud,C., Marcel,F., Souillet,Y., Borel,E., Gebuhrer,L., Santoro,L., Marcel,S., Seigneurin,J.M., Marche,D.N. and Lafon,M.
Multiple sclerosis retrovirus particles and recombinant envelope trigger an abnormal immune response in vitro, by inducing polyclonal Vbetal6 T-lymphocyte activation
Virology 287 (2), 321-332 (2001)
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                                                                                                                                                                                                                                                                   1 (bases 1 to 1629)
Perron, H., Ounanian-Paraz, A., Marcel, F. and Souillet, Y.
Direct Submission
Submitted (21-DEC-2000) R&D, bioMerieux, Chemin de L'Orr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="surface and transmembrane regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1461.8;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:89382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Multiple
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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1. .1629
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Best Local Similarity 99.2%;
Matches 1469; Conservative (
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1. .1629
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1 (bases 1 to 1629)
Perron, H., Jouvin-Marche, E., Michel, M., Ounanian-Paraz, A.,
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                                                                                                               AC023366 172918 bp DNA linear HTG 02-MAR-2000
Homo sapiens clone RP11-15N10, WORKING DRAFT SEQUENCE, 33 unordered
pieces.
                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 172918)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (14-FEB-2000) Whitehead Institute/MIT Center fo
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 2, 2000 this sequence version replaced gi:6970363.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project name: Li3492
Center clone name: 15_N 10
Center clone name: 15_N 10
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 156863 bases at least Q10
Consensus quality: 156863 bases at least Q20
Consensus quality: 164107 bases at least Q20
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Insert size: 169718; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; agarose-fp
Quality coverage: 3.0 in Q20 bases; sum-of-contigs
1441 GAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCA 1481
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Unpublished
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HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
Homo sapiens
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KEYWORDS
SOURCE
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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FEATURES source

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Clone_lib="RPCI-11 Human Male BAC"
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98.7%; Score 1461.8;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches
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Mallet,F., Bouton,O., Prudhomme,S., and Mandrand,B.
Bonnand,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
14757826
                                                                          Gorilla gorilla isolate 1 endogenous retrovirus ERV-W, ERVWE1 AV101589
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Gorilla gorilla

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

1 (bases 1 to 10230)
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.larity 94.1%; Pred. No. 0;
Conservative 0; Mismatches
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AUTHORS
TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                             SOURCE INFORMATION:
The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA was isolated from white blood cells obtained from a male chimpanzee (pan troglodytes, 'Clint', Yerkes #C0471; birthdate: 6-6-80). The clone and detailed information can be obtained from ResGen (http://www.resgen.com) or Pieter de Jong and co-workers at http://www.bacpac.chori.org.
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                                                                                                                                                                                  MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu
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                                                                 This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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RSDVNDIKGTPPEELLTAQQPLRRPNSAGSS"
                                                                  Pan troglodytes isolate 1 endogenous retrovirus ERV-W, ERVWE1 locus, allele A, complete sequence.
AY101586.1 GI:37544407
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Mallet, F., Boutom, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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join(1248. .810,2889. .9820)

join(1248. .810,7592. .9820)

join(248. .810,7592. .9820)

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fproduct="envelope alycoprotein"

join(248. .810,9255. .9820)

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fnoce="putative mRNA transcript 3; no coding region"

fnoce="syncytin"
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/cell_type="pBMC"
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
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Best Local Similarity 94.1%;
Matches 1393; Conservative
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                                                                                                ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTC 1320
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1 (bases 1 to 10229)
Mallet, F., Bouton, O., Pudhomme, S., Cheynet, V., Oriol, G., Mallet, F., Bouton, O., Duret, L. and Mandrand, B. Lucotte, G., Duret, L. and Mandrand, B. The endogenous retroviral locus ERVWEl is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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                                                                                                                                                                        GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA
                                                        ATTCGAGATCGAATACAACGTAGAGCAGAGGAGCTTCGAAACACTGGACCCTGGGGCCTC
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Maller,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (06-MAY-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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1. 778
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/note="putative mRNA transcript 2"
/note="putative mRNA transcript 2"
/note="putative mRNA transcript 3; no coding reg
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90.5%; Score 1340.2;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1393; Conservative 0; Mismatches
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/ codon start=1
/ codon start=1
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/ product="envelope glycoprotein"
/ product="envelope glycoprotein"
/ product="envelope glycoprotein"
/ product="envelope glycoprotein"
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HTRLVSLFNTTLTGLHEVSAQNPTNCWICLPLDFRPYVSIPVDGTVCLPSGIFFVGGTSA
TVGPLVSULBITHTSNLTCWKENTIDTTNSQCIRWTTPPTQLVCLPSGIFFVGGTSA
YRCLNGSSESMCFLSFLVPPWITTTTGQDLYNYVSKPRNKRVPILPFVIGAGVLGALG
TGGGTTGSTQFYYKLSGELNGDMBRVADSLYTLQOQLNSLAANVLQNRRALDLLTAB
TGGTCLFLGEBCCYYVNQSGIVTEKVKEIRDRIQREAELRATGPWGLLSQWMPWILP
FLGPLAALILLLEGGPCIFNLLVNFVSSRIBAVKLQMBFKMQSKTKIYRRPLDRPASP
RSDVNDIKCTPPEEISTAQPLLRPNSAGSS"
9497. .10230
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join(248. 826,7595. 9821)
/product="envelope glycoprotein"
/note="putative mRNA transcript 2"
join(248. 826,9258. 9821)
/note="putative mRNA transcript 3; no coding region"
7822. 9438
/note="syncytin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10230;
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                                                                                                                                                             ERVWE1 locus, allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGCCCTCCCTTATCATACTTTTCTCTTTACTGTTCTCTTTACCCCTTT
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1. 10230
/organism="Gorilla gorilla"
/mol type="genomic DNA"
/isolate="1"
/isolation source="PBMC of go
/db xref="taxon:9593"
/cell type="PBMC"
/note="isolated by PCR; ERUWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1340.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                           endogenous virus: ERV-W"
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Best Local Similarity 94.1%;
Matches 1393; Conservative
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Gorilla gorilla

Gorilla gorilla

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

1 (bases 1 to 10230)

Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,

Mallet, F., Ductet, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gorilla gorilla isolate 1 endogenous retrovirus ERV-W, ERVWE1 locus, allele A, complete sequence.
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      ATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCTCAGCCTATCGTTGTTTG 8658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGAAGAATGCTGTTATGTTAATCAATCCGGAATCGTCACTGAGAAGTTAAAGAA 9078
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                                                                          AATGGCTCTTCAGAATCTATGTGCTTCCTCTTCTTAGTGCCCCCTATGACCATCTAC
                                                                                                                                                               ACTGAACAAGATTTATACAATTATGTCGTATCTAAGCCCCGCAACAAAAGAGTACCCATT
                                                                                                                                                                                                                                                                                                                    GTGGCCGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
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                                                                                                                                        ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCCACAAAAGAGTACCCATT
                                                                                                                                                                                                                                CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC
                                                                                                                                                                                                                                                                        crrccrrrrgranagaagcagagrecraggrecacraggracregcarregegrare
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                                                                                                                                                                                                                                                                                                                                                                                                            GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
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Direct Submission
Submitted (16-MAY-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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                               CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTCAATC
                                                                       CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA
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AY101593 10-FBB-2004 Hylobates pileatus isolate 1 endogenous retrovirus ERV-W, ERVWE1 locus, allele B, complete sequence.

RESULT 17 AY101593 LOCUS DEFINITION

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GNIDAPLYRSFSKGSPTFTAHTYMPRICYRGATLCHANTOYWTGKNINPSCPGGLGY
TVCWTYPFHTGMSDGGGVQDQAREKHVKEVISQLTCWHANTOYWTGKNINPSCPGGLGY
TVCWTYPFHTGMSDGGGVQDQAREKHVKEVISQLTCWHSTSSPYKGLDLSKLHETLKT
HTRLVSLFNTTLTGLHEVSAQNPTWCMCLPLDFRPYSSIPVEDWNHSTSTELNTTSV
VPCBAUSGSTSKOFFLSFUYPPWTIYTEQDLTWYVOKTPRNETFLTFPUTSGVTGGLG
TGIGSITTSTQPYYKLSRELNGDMRRYADSLYTLQDQLNSLAAVULQNRAALDLTAB
FGGTCLFIGEBCCYYNNGSGTIYTEKVEIRDRIQARABELLAB
FLGPLAAIILLLLFGGCIFWLLNNFVSSRIRAIKLQMBPKMSSKTKNYRRSLDWPAILP
RSDVNDTKGIPPERISTAQPLLRPNSAGSS"
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Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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                                              Hylobates pileatus (pileated gibbon)
Hylobates pileatus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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Direct Submission

Submitted (O6-MAY-2002) Retrovirology Department, UMR 2142

CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6334 cedex 07, France
Location/Qualifiers
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1. 773

join(248. .254,2843. .9807)

join(248. .254,7579. .9807)

/product="revelope glycoprotein"

join(248. .254,9242. .9807)

/note="putative mRNA transcript 2"

join(248. .254,9242. .9807)
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/protein_id="AAM68172.1"
/db_xref="Gl:37544422"
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Pred. No. 0;
0; Mismatches
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/db_xref="taxon:9589"
/cell_type="PBMC"
/note="isolated_by_PCR;
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/note="syncytin"
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Best Local Similarity 94.0%;
Matches 1392; Conservative
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AY101593.1
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AF520477S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 132 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence. AF520478 AF520478 GI:33410924
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CTTCCTTTTGTTATCAGAGCAGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC
           GTCACTGCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
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- 46 allee
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Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMersleux, Escle Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/mol_type="genomic_DNA"
/mol_type="individual 132 allele
/db.xref="taxon:9606"
/chromosome="7"
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/organism="Homo sapiens"
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/sex="female"
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9483. .10248
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                                                                    AGCAATACTACATACACCAACTCCCCAATGCATCAGGTGGGTAACTCCTCCCACACAA
                                                                                                                       AATGGCTCTTCAGAATCTATGTGCTTCCTCATTCTTAGTGCCCCCTATGACATCAAC
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                          GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT
                                                                                                                                                                AATGGCTCTTCAGAATCTATGTGCTTCCTCATTCTTAGTGCCCCCTATGACCATCTAC
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GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT
                                                    AGCAATACTATAGACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACACGA
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GNIDABSYRSLSKGTPTFTAHTHMPRNCYHSATLCKHANTHYWTGKNINPSCPGGLGV
CWWYPYTOTGKASDGGGVQDAREKTWEVISQLTRVHGTSSPYGEDLSKLHETLETH
HTRLVSLENTTLTGHEWSAQNPTHOWICLPINFRPYVSIPPPEDLSKTHETLETH
TYRCLNGSESWFELSTUPPWTIYTTGDLXWYFPTQIVCLPSGIFFVCGTSA
YRCLNGSSESWFELSFLVPPWTIYTTGDDLXNYYISKPRNFRYPTILPFVIGAGVIGALG
TGIGGITTSTQPYYKLSGLNGDMFRVADSLYTLQDQLNSLAAVILQNRRALDLLTAE
RGGTCLFLGEECCYYNQSGIVTBKWEIRDRIQRRAEELRYTGPWGLLSOMMPWILP
FLGFLAAIILLFGPCIFULVNFVSSRIEAVKLQMERAELRYTGPWGLLSOMMPWILP
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                                                               /note="8yncytin"
/codon_start=1
/product="envelope glycoprotein"
/protein_id="AAQ1761.1"
/db_xref="GI:33410925"
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/note="splice acceptor site"
1959. .2694
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Pred. No. 0;
0; Mismatches
           endogenous_virus: HERV-W"
                                   /note="splice acceptor 284. .1900
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AF520487S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 148 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence. AF520488 Craniata, Vertebrata, Euteleostomi, Catarrhini, Hominidae, Homo. 2 of 2
Homo sapiens (human)
Homo sapiens
Exaryotes; Metazoa; Chordata; Craniata; Vertebrata; Butel,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.

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             AGCACCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC
                                                         CATACTOGCCTGGTGAGCCTATTTAATACCACCTCACTCGGCTCCATGAGGTCTCAGCC
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CAAGGTCAGGCAAGAGAAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACAT
                                                                                                           CATACTCGCCTGGTAAGCCTATTTAATACCACCTCACGGGCTCCATGAGGTCTCGGCC
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- 46 allee
    The endogenous retroviral locus ERVWE1 is a bona fide gene in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
14757826
2 (bases 1 to 2694)
Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (07-JUM-2002) Retrovirology Department, UMR 2142 (CNRS-biowderieux, Ecole Normale Superieure de Lyon - 46 alled 'Italie, Lyon 69364 cedex 07, France
      locus ERVWE1 is a bona fide gene
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/isolate="individual 148 allele
/db_xref="taxon:9606"
/chromosome="7"
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/product="envelope glycoprotein"
/protein_id="AAQ17566.1"
/db_xref="GI:33410945"
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/note="splice acceptor site"
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/note="splice acceptor site"
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Pred. No. 0;
0; Mismatches
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/note="Caucasian
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/note="syncytin"
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Direct Submission
Submirted (Or-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
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/mol_type="genomic DNA"
/isolate="individual 22 allele A'/db xref="taxon:9606"
/chromosome="7"
/map="721.q22"
/sex="male"
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/note="syncytin"
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RGGTCLFLGEBCCYYVNOSGINYBEKVKEIRDRIQKRAEELENTGPWGLLSQWMPWILD
FLGPPLAAILLLLEGPCIFNLLVNFVSSRIEAVKLQMEPKMGSKTKIYRRPLDRFASP
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1 (bases 1 to 2694)

Mallet, F., Bouton, O., Prudhowme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWEl is a bona fide gene involve in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
             CAAAATCGAAGGTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTATTA
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeritux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69346 cedex 07, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481
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mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 alle
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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AUTHORS
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1. .2694
/organism="Homo sapiens"
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284. .1900

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2694)
                                          Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G., Bonnaud,B., Incotte,G., Duret,L. and Mandrand,B.
He endogenous retroviral locus ERVWE1 is a bona fide gene in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                       Allet.F. Bouton.O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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Length 2694;
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                              Indels
 6
                              91;
 DB
Score 1335.4;
Pred. No. 0;
0; Mismatches
90.2%;
nilarity 93.9%;
Conservative 0
                   Best Local Similarity
Matches 1390; Conserv
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AF520520.1 GI:33411008 2 of 2 Homo sapiens (human) Homo sapiens

ACCESSION VERSION KEYWORDS SEGMENT SOURCE ORGANISM

LOCUS RESULT 24 AF520519S2

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AF520521S2

2694 bp DNA linear PRI 11-FEB-2004
Homo sapiens individual 6 allele A, envelope glycoprotein gene,
complete cds, and 3' long terminal repeat, complete sequence.
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Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEl is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 93.9%;
Matches 1390; Conservative
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Direct Submission
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I (bases 1 to 2694)

Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.

The endogenous retroviral locus ERVWEl is a bona fide gene involve in hominoid placental physiology

Proc. Natl. Acad Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Maller,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
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/codon_start=1
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/product="envelope glycoprotein"
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TG1GGITTSTGPTCFXLSPLYPWTYTTNSQCIRWTPPTQ1VCLPSGIFFVCGTSA
YRCLNGSSESGNCFLSFLYPWTYTTNSQLYNTVICOLNSILAAVLQNRRALDLLTAE
RGGTCLPGEECCYYVNQSGIVTEKVWEIRDRIQRRAEELRNTGPWGLLSQMMPWILP
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RSDVNDIKGTPPFEISAAQPLLRPNSGSS"
/note="splice acceptor site"
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                                               /organism="Homo sapiens"
/mol type="genomic DNA"
/isolate="individual 71 allele A'
/db_xref="taxon:9606"
/chromosome="7"
/map="7921-922"
/sex="male"
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Lyon 69364 cedex 07, France Location/Qualifiers
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Pred. No. 0;
0; Mismatches
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/note="splice acceptor site"
                                                                                                                                                                                    endogenous_virus: HERV-W"
                                                                                                                                                        /cell_type="PBMC's"
/note="African
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                CAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCAGGCCATACATTTCAATC
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                                                                              CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA
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HTRLVSLFNTTLTGLHEVSAQNPTNCWICLPLNFRPYVSIPVPEQWNNFSTEINTTSV
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                                           Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                        treating preeclampsia
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                                                                                                      Keith, J.C., Mccoy, J.M. and Mi,S.
Methods and compositions for diagnosing and and gestational trophoblast disorders
Patent: WO 0204678-A 1 J7-JAN-2002;
GENETICS INSTITUTE, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.2%; Score 1335.4; DB 6; 93.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                930. .2546
/note="unnamed protein product"
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/db_xref="taxon:9606"
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Mi,S., Lee,X., Li,X., Veldman,G.M., Finnerty,H., Racie,L., LaVallie,E., Tang,X.Y., Edouard,P., Howes,S., Keith,J.C. Jr. and
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LaVallie,E., Tang,X., Edouard,P., Howes,S., Keith,J.C. Jr. and
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Direct Submission
Submitted (26-NOV-1999) Genetics Institute, 87 Cambridge Park
Drive, Cambridge, MA 02140, USA
Location/Qualifiers
                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="laxon:9606"
/clone="AJ172-28"
/tissue_type="testis"
1.2930
/rpt_family="Human endogeneous retrovirus HERV-W"
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/note="furin; cleavage site"
/evidence=not_experimental
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Nature 403 (6771), 785-789 (2000)
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/product="syncytin"
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          Homo sapiens (human)
Homo sapiens
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Best Local Similarity 93.9
Matches 1390; Conservative
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1348 GGCACCTCTAGACGACTAGATCTCTCAAAACTACATGAAACCTCGGTACC 1407	Qy 721 AGCAATACTATAGACACCAGCTCCCAATGCATCAGGTGGTGACACCCTCCCACAGG 780 Db 1648 AGCAATACTACAACCAACCACTCCCAATGCATCAGGTGGTAACTCCTCCCCACACAA 1701 Db 1781 ATAGTCTGCTACCCTCAGGAATATTTTTTTTTTTTTTTT	1021 ACAACCTCTACTCAGTTCTACAAACTATCTCAAGAAATAAAT	00 00 00 00 00 00 00 0	1381 TTACTCCTCTTTGGACCCTGTATCTTT 2308 CTACTCCTCTTTGGACCCTGTATCTTT 1441 GAAGCTGTAAAGCTACAGATGGTCTTA 2368 GAAGCTGTAAAACTACAAATGGAGCCC	Search completed: January 22, 2005, 16:13:53 Job time : 6221.46 secs
Oy 1261 ATTCGAGATCGAATACAATGTAGAGCAGAGCTTCAAAACACCGAACGCTGGGCCTC 1320	RESULT 30 AR177269 LOCUS AR177269 LOCUS AR177269 LOCUS ACCESSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION ONCLOSSIFIED ONCLOSSIFIED AR177269 VERSION AR177269 AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 VERSION AR177269 AR1772	Query Match 90.2%; Score 1335.4; DB 6; Length 2946; Best Local Similarity 93.9%; Pred. No. 0; No. 0; Matches 1390; Conservative 0; Mismatches 91; Indels 0; Gaps 0; Qy 1 ATGGCCCTCCTTATCATTTTCTTTTACTGTTCTTTACCCCTTTTACCTCTTCACTCTCTCT	Oy 121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATGGAGTTTATCTAAGGGAAACTCC 180 1048 ATGCAGCGTCCCGGAAATATTGATGCCCCATCGTATAGGAGTTTTCTAAGGGAACCCC 1107 Oy 181 ACCTTCACTGCCCACCCATATGCCCCGCAACTGCTATACTCTGCCACTCTTTGCATG 240 1108 ACCTTCACTGCCCACCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG 120 Oy 241 CATGCAAATACTCATTATTGCACCGGAACATCATAATCCTAGTGCCACTCTTTGCATG 1167 Oy 241 CATGCAAATACTCATTATTGCACAAAAATAATACTAGTTGTCCTGGAGGACTT 300 1168 ACCTTCACTGTATATTGGACAAGGAAAATAATACTAGTTGTCCTGGAGGACTT 1207 O	301 GGAGCCACTGTTGTTGACTTACTTCACCCATACCAGTATGTTGTGTGGGGGGGG	Qy 421 AGCACCCCTAGCACAGGACTAGTTCTCTCAAAACTACATGAAACCTCCGTACC 480

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January 22, 2005, 11:11:14; Search time 679.669 Seconds (without alignments) 11438.492 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ΠD	Description
1	1481	100.0	1481	7	AAV43217	Aav43217 Multiple
7	1481	100.0	1481	7	AAX29703	Aax29703 Clone C15
e	1481	100.0	1481	12	ADG14846	Adg14846 MSRV asso
4	1481	100.0	2030	m	AAA63826	Aaa63826 Nucleotid
ഗ	1461.8	98.7	1629	٣	AAA96625	Aaa96625 DNA encod
9	1450	97.9	1481	6	ADB84400	Adb84400 MSRV-1 as
7	1389.8	93.8	2074	9	AAD41225	Aad41225 Human EMB
80	1335.4	90.2	2930	9	AAD24195	Aad24195 Human syn
6	1335.4	90.2	2946	7	AAX77526	Aax77526 Human sec
10	1335.4	90.2	2946	m	AAZ59468	Aaz59468 Human sec
11	1335.4	90.2	2946	10	ADC38776	Adc38776 Human cDN
12	1333.8	90.1	1617	ហ	AAH20070	Aah20070 HERV-W en
13	1333.8	90.1	2055	٣	ABN97948	Abn97948 Human ret
14	1333.8	90.1	2599	ო	ABN97927	Abn97927 Human ret
15	1333.8	90.1	10499	n	ABN97929	-
16	1333.8	90.1	56093	ø	ABL61744	_
17	1330.6	89.8	2781	Ŋ	AAF55630	Aaf55630 Nucleotid
18	1324.2	89.4	7582	е	AAA59215	Aaa59215 Human end
19	1322.6	89.3	7582	7	AAX25665	Aax25665 Complete
20	1308.2	88.3	2782	Ŋ	AAH20069	Aah20069 HERV-W en
21	1306.6	88.2	2782	7	AAX25661	Aax25661 Human end

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P-PSDB; AAW99553.
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The present sequence represents a multiple sclerosis (MS) associated retrovirus (MSRV) genomic fragment used in the method of the invention. The invention provides complete or partial genomic sequences of the MSRV-1 pol gene, gag gene and env gene, and polypeptides encoded by these genes. The invention also provides antibodies raised against the polypeptides. The genomic sequences, polypeptides and antibodies are also claimed useful for diagnosing infection by MS and rheumatoid arthritis-associated viruses, and also for prevention and treatment of infection with these viruses
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                                                                                   This sequence represents clone C15 from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-ANG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field.)
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                Nucleic acid sequences of retrovirus called MSRV-1 multiple sclerosis or rheumatoid polyarthritis.
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                                                                                                                                                                                                                                set Local Similarity 100.0%; Score 1481; set Local Similarity 100.0%; Pred. No. 0; Atches 1481; Conservative 0; Mismatches
                                                              Claim 1; Page 37-38; 83pp; French
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 AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACACAA
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                                                          New isolated nucleic acid and their fragments having the pol gene of a retrovirus, useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis.
                                                                                                                                             The invention relates to an isolated nucleic acid which comprises the gene of a retrovirus associated with multiple sclerosis or rheumatoid arthritis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis. The present sequence is used in the exemplification of the invention.
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                                                                                                                      Disclosure; SEQ ID NO 105; 193pp; English
       Jolivet-Reynaud C,
                                    WPI; 2004-032461/03
        Komurian-Pradel F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes an envelope protein of MSRV-1. The envelope protein expressed by the endogenous human retrovirus MRSV-1 has be protein expressed by the endogenous human retrovirus MRSV-1 has be detected using the method of the invention. The specification describes a process for detecting activity of a superantigen in a biological sample. The process comprises identifying large scale expansion or loss of lymphocytes that carry at least one of the Wobtal6 and/or Wobtal7 determinants. The method is used to screen for agents that inhibit the superantigen, especially those associated with MRSV-1 which is implicated in autoimmune disease, particularly multiple sclerosis.

These agents are potentially useful for treatment or prevention (e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting superantigen activity, useful for identifying agents for treatment or prevention of autoimmune disease, from expansion or loss particular lymphocyte Vbeta determinants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GCACCCCCCCCATGCTGCTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGCCCTCCCTTATCATACTTTTCTCTTTACTGTTCTCTTTACCCCCTTTCGCTCTCACT
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                                                                                                                                                                                                  Envelope protein; MSRV-1; superantigen; autoimmune disease; Vbeta16;
Vbeta17; multiple sclerosis; vaccine; ss.
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 1441 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481
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                                                                                                                                                                      an envelope (env) protein of MSRV-1.
                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .1629
/*tag= a
/product= "envelope protein"
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              These agents are potentially use: vaccines) of autoimmune diseases
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                                                                           standard; DNA; 1629
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99FR-00013755
                                                                                                                                                                                                                                              Human endogenous retrovirus
                                                                                                                                      (first entry)
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Matches 1469; Conservative
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                                                                                                                                                                  DNA encoding
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28-OCT-1999;
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GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated or purified nucleic acid from a virus associated with multiple sclerosis and/or rheumatoid arthritis, multiple sclerosiated virus (MSRV)-1. The nucleic acids comprise pol, gas or reverse transcriptase genes (or their fragments) encoding the proteins or defined peptides (including immunodominant peptides, antigenic peptides or conserved motifs). Also included are a process for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample, a nucleic acid probe for the detection of a virus associated with multiple sclerosis or rheumatoid arthritis, a primer for the amplification by polymerisation of a nucleic acid of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
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                                                                           CTCAGCCAATGGATGCCCTGGACTCTCCCCTTTAGGACCTCTAGGCAGCTATATTT
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                                  CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG
                                                                                                                                TTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAATT
                                                                                                           TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT
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                                                                                                                                                                                                                                                                                                                    ds; multiple sclerosis; rheumatoid arthritis; gag; pol; reverse transcriptase; ribonuclease H.
                                                                                                                                                     GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481
                                                                                                                                                               Paranhos-Baccala G;
aud C, Mandrand B,
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adel F, Jolivet-Reynaud
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PARANHOS-BACCALA G.
KOMURIAN-PRADEL P.
JOLIVET-REYNAUD C.
MANDRAND B.
GARSON J. A.
TUKE P. W. J. A.
                                                                                                                                                                                                                                                                           (first entry)
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BESEME F.
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viral material associated with multiple sclerosis or rheumatoid arthritis, a polypeptide exhibiting an inhibitory activity on the proteolytic, reverse transcriptase or ribonuclease H activity from MSRV, and antibody directed against the MSRV-1 virus obtained by immunologically reacting a human or animal body or cells with an immunopolic agent consisting of the antigenic polypeptide defined above. The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis, or for detecting in a biological sample, the presence of or exposure to a virus associated with multiple sclerosis or rheumatoid arthritis. The present sequence is a claimed MSRV-associated sequence whose identity cannot be accurately determined. Note: The SEQ ID numbers for the sequences as displayed in the main body of the patent do not match the SEQ ID numbers in the sequence listing. Consequently those sequences mentioned in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 CATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Length 1481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1450; DB 9; Pred. No. 0; 0; Mismatches 3
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Best Local Similarity 97.9
Matches 1450; Conservative
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                       GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
                                                 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC
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         ATAGICTGCCTACCCTCAGGAATATTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTG
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The invention relates to human embryogenesis associated proteins (EMBRY) and nucleic acid molecules encoding such proteins. EMBRY sequences are useful for screening modulators useful for treating or preventing disorders associated with abnormal expression of EMBRY. The disorders treated include reproductive disorders such as infertility, endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory disorder such as acquired immune deficiency syndrome (AIDS), allergies, contact dermatitis; disorders of the placenta such as precelampsia, abruptio placentae etc. Sequences of the invention are also useful for analysing a proteome of a tissue or a cell type. EMBRY proteins are useful as immunogens for preparing antibodies. Polynucleotides of the invention are useful for creating knockin humanised animals or transgenic animals to model human diseases. They are also used in gene therapy. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptides of human embryogenesis associated proteins for screening modulators useful for treating or preventing disorders e.g.
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                                                                                          "Mature EMBRY-2 protein"
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Best Local Similarity 96.2%;
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syncytin expression. The syncytin modulators are useful in diagnosis and treatment of preclampsia and gestational trophoblast disorders (e.g. choriocarcinoma, hydatiform mole, placental site tumour and missed/ incomplete abortion). Syncytin is a human gene derived from the envelope gene of human endogenous defective retrovirus, HERV-W. The present invention is based partly on the discovery that syncytin expression is dramatically reduced in preeclampsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a compound for treating a subject with or at risk of eveloping preeclampaia, comprises determining whether the expression or activity of syncytin in the cell is modulated in the presence of a test compound.
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                                                                                                                                                                                                                             syncytin; preeclampsia; gestational trophoblast disorder; carcinoma; hydatiform mole; placental site tumour; abortion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein; testes; brain; blood; placenta; human; murine; thymus; bone marrow; treatment; prevention; nutrition; cytokine; immune; vaccine; cell proliferation; cell differentiation; suppressor; tumour inhibition; haematopoiesis regulator; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.
                                                                                                                                                                                                  1381 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; disease diagnosis; pre-eclampsia; cancer; placental pathology; metastasis inhibition; nutritional activity; immune stimulator; hamatopoiesis regulator; tissue growth; tumour inhibitor; anti-inflammatory; clone AJ172_2; ATCC_98115;
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autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; allergic reaction; asthma; myeloid cell deficiency; rhymboid cell deficiency; osteoportosis; osteoarthritis; peripheral nervous system disease; peripheral neuropathy; Alzheimer's disease; Parkinson's disease; coagulation disorder; inflammatory disease; Parkinson's disease; coagulation disorder; ischaemia-repertusion injury; Czohn's disease; anaphylaxis; hypersensitivity; regeneration; neural cell proliferation; fertility;
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                          This is the human secreted protein AJ172 2 nucleotide sequence, obtained from a human adult testes CDNA library. The invention relates to secreted human and mutrine proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for an imal preventing or ameliorating medical conditions in humans and treating, preventing or ameliorating medical conditions in humans and diagnosis of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity, (e.g. in feeds), cytokine and coll proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemacopiesis regulating activity, chemotactic/chemokinetic activity, haemacopiesis regulating activity, chemotactic/chemokinetic activity, haemacotatic and thrombolytic activity, creeptor/ligand activity, and tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotide sequences are also stated to be useful for gene therapy
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93.9%; Pred. No. 0;
iive 0; Mismatches
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Jacobs K, Mccoy JM, Lavallie BR, Collins-Racie LA, Evans C;
Merberg D, Treacy M, Bowman MR, Spaulding V, Carlin-Duckett M;
Kelleher K;
tumour; chemokine; human; secreted protein.
                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 134; 412pp; English
                                                                                                                 960S-00721488.
960S-00721798.
960S-00721923.
960S-00738367.
960S-00739775.
970S-00833823.
970S-00833823.
                                                                     96US-00628364.
96US-00635311.
96US-00659224.
96US-00664596.
96US-00677231.
96US-0068678.
                                                  02-APR-2002; 2002US-00114893
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                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                       WPI; 2003-657236/62
                                                                                                                                                                                                                                             P-PSDB; ADC38777.
                          US2002193567-A1
             Homo sapiens
                                      19-DEC-2002
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23-AUG-1996
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27-SEP-1996
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19-APR-1996
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The invention relates to a protein comprising fully defined AZ302 1 protein or BD127 1 6 protein. The polynucleotides are useful for protein or BD127 1 6 protein. The polynucleotides are useful for capressing recombinant proteins for analysis and are also useful as chromosome markers or tags to identify chromosomes or to map related gene positions. The proteins are useful as amino acid supplement, carbon source, nitrogen source and carbohydrate source. The proteins are useful for treating various immune deficiencies and disorders (e.g. multiple combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple comporosis, systemic lupus errythematosus, rheumacoid arthritis), allergic reactions (e.g. asthma), myeloid or lymphoid cell deficiencies, osteoporosis or osteoarthritis, pertipheral nervous system disease), coteoporosis or osteoarthritis, pertipheral nervous systemic inflammatory response syndrome (SIRS), ischaemia-repertusion injury, Crohn's disease), coagulation disorders, inflammatory diseases (e.g. systemic inflammatory response syndrome (SIRS), ischaemia-repertusion injury, Crohn's disease), anaphylaxis and hypersensitivity. Proteins are also useful for inducing tumour immunity, for inducing bone, cartilage, tendon, ligament and/or nerve growth or regeneration, for proliferating nerva and brain tissue, for inducing fertility and for inhibiting tumour growth. Proteins are also useful as chemckine for mammalian cells (e.g., monocytes, fibroblasts, neutrophils), and also useful as inhibitors of receptor/ligand interactions. The present sequence represents cDNA encoding a human secreted protein. Proteins A23021 encoded by clone A23021 from human adult colon, and BD12716 encoded by clone BD12716 from human fetal kidney cDNA library, useful for treating e.g. multiple sclerosis and rheumatoid arthritis.

Sequence 2946 BP; 858 A; 801 C; 570 G; 717 T; 0 U; 0 Other;

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2946	°;
Length	Indels
DB 10;	91;
90.2%; Score 1335.4; 93.9%; Pred. No. 0;	0; Mismatches
Query Match 90.2%; Best Local Similarity 93.9%;	Matches 1390; Conservative

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ò	61	CCCTCCATGCTGCTGTACCAGCAGTAGCTCCCCTTACCAAGAGTTT
Q Q	988	CACCCCTCCATGCTATGACCAGTAGCTCCCCTTACCAAGAGTTTCTATGGAGA 10
'n	21	ATATAGGAGTTTATCTAAGGGAAACTCC 180
DP DP	1048	CCGGAAATATTGATGCCCCATCGTATAGGAGTCTTTCTAAGGGAACCCCC 11
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අු	90	cactigeceacacecatatigececedaetigetateaeteteceaetettigeatig 11
දු පු	241	CATGCAAATACTCATTATTGGACAGGGAAATGATTATTCCTAGTTGTCTGGAGGACTT 300
λ̈	301	ACTGTCTGTTGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGTGGAATT 36
q	1228	
ò	361	42
qq	1288	
λ̈	421	CTCAAAACTACATGAAACCCTCCGTACC 48
QQ Q	1348	CACCTCTAGGCCCCTACAAAGGACTAGATCTCTCAAAACTACATGAAACCCTCGGTACC 14
ò	81	CCTCACTCGGCTCCATGAGGTCTCAGCC 54
q	1408	TCGCCTGGTAAGCCTATTTAATACCACCCTCACTGGGCTCCATGAGGTCTCGGCC 14
λ	541	TTCAATC 6
g	9	CAAAACCCTAACTAACTGTTGGATATGCCTCCCCTGAACTTCAGGCCATATGTTTCAATC 1527
à	601	CCIGITCCIGAACAATGGAACAACITCAGCACAGAAATAAACACCACITCCGIITITAGIA 660
පි	1528	CCTGTACCTGAACAATGGAACAACTTCAGCACAGAATAAACACCCACTTCCGTTTTAGTA 1587
ò	661	20
g	1588	GGACCTCTTGTTTCCAATCTGGAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT 1647
à	721	AGGAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACACGA 780
원	1648	AGCAATACTACATACACAACCAACCCAATGCATCAGGTGGGTAACTCCTCCCACAAA 1707
à	781	8
a	1708	rerrre 17
à	841	AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC 900
eg G	1768	TITCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC 18
à	901	ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACAACAAAAGAGTACCCATT 960
Q	1828	ACTGAACAAGATTTATACAATTATGTCATATCTAAGCCCCGCAACAAAGAGTACCCATT 1887
à	961 (102
g	1888	STITTGITATAGGAGGAGGAGTGCTAGGTGCACTAGGTACTGGCATTGGCGGTATC 194
à	021	20
q	48	caaccroracticagirciaciacaacrarcicaagaaciaaargeegacargaaggg 200

us-09-319-156b-9.rng

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cc was been located on the long arm of human chromosome 7 (7q21-22) has been designated HERV-W. The present invention describes proteins or peptides (1) having superantigen (SAg) activity comprising the ENV protein (BNV) of HERV-W, the surface protein (SU) and transmembrane (TN) sub-units. (I) have neuroprotective activity, and can be used in: vaccines; antisensetherapy; and HERV-W SAg activity-inhibitors. (I) and encoding DNA/RNA are useful for idangosing multiple sclerosis (MS) or HERV-W-associated disorders. (I) are also useful for identifying substances (and optionally recovering) capable of binding to a retroviral superantigen associated with MS, substances capable of blocking sAg activity and substances capable of blocking transcription or translation of HERV-W retroviral superantigen. A protein or peptide derived from (I), modified to be gainst HERV-W retroviral SAg is useful in therapy. Nucleic acid molecules encoding (I) are useful as vaccines against MS. Substances capable of blocking transcription or translation of HERV-W retroviral superantigen for use in treating or translation of HERV-W retroviral superantigen for use in treating or preventing MS. Obtained using (I) are useful for the treatment and corrective prevention of MS. (I) and nucleic acids encoding them are useful for diagnosing autoimmune disease. The present sequence encodes the specifically claimed envelope protein of HERV-W designated G specifically claimed envelope protein of HERV-W designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCACCCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1333.8;
Pred. No. 0;
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Best Local Similarity 93.8
Matches 1389; Conservative
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endogenous retrovirus (HERVs) the full length endogenous provirus which
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                  GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
                                        GTCGCCGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein; envelope protein; multiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective; antisense-therapy; autoimmune disorder; ds.
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                                                                                                                                              chromosome 7q; immunotherapy;
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                                 ABN97948 standard; DNA; 2055
                                                                                                                                             Autoimmune disease; HERV-7q;
                                                                                                                                                                                        Human endogenous retrovirus.
                                                                                       (first entry)
                                                                                                                                                             multiple sclerosis;
                                                                                                                                                                                                                  WO9967395-A1
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CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC

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The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. equilatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immune response, e.g. in immunotencic or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was used to illustrate the invention
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                                                                                                                                                                                                                                                                                          New nucleic acid sequences of human endogenous retrovirus, HERV-7q, used for diagnosis, treatment and prevention of autoimmune and neurological
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Pred. No. 0;
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99WO-FR001513
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Best Local Similarity 93.8%;
Matches 1389; Conservative
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7q; immunotherapy;

HERV-7q; chromosome

Autoimmune disease; multiple sclerosis; Human endogenous retrovirus

sequence HERV

retroviral

Human

(first entry)

01-AUG-2002

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

99WO-FR001513

23-JUN-1999; 23-JUN-1998;

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29-DEC-1999.

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Best Local Similarity 93.8%;
Matches 1389; Conservative
PM, Perin J,
                                    WPI; 2000-160587/14.
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90.1%; Score 1333.8; DB 3; Length 10499;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 1389; Conservative 0; Mismatches 92; Indels 0:
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                         TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATT
                                                   CTAGCAGCTCTAATATTG
                       crcagecaaregarececregarrerececrireraggaecererageageraraararre
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                                                                               GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481
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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent cobe tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises in indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating doutal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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Best Local Similarity 93.8%;
Matches 1389; Conservative 121 181 241 301 61 361 35939 35999 36059 36119 36179 g 요 Q 셤 ઠે ò ò g 셤 셤 ò ઠ ઠે ઠ

RESULT

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36658 36718 1381 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440 840 960 ATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCTCAGCCTATCGTTGTTTG 36299 GGCACCTCTAGCCCCTACAAGGACTAGATCTCTCAAAACTACATGAAACCCTCCGTACC 36479 CCTGTACCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC 86959 GTCGCCGACTCCCTGGTCACGTTGAACTTAACTCCCTAGCAGCAGTAGTCCTT CTCAGCCAATGGATGCCCTGGATTCTCCCCCTTCTTAGGACCTCTAGCAGCTATAATAGTTG CTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCTTCCAGAATC caracteceregraageerarrraaraceaeeereaeregeerecargagereregeee CAAAACCCTACTAACTGTTGGATATGCCTCCCCTGAACTTCAGGCCATATGTTTCAATC CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACACA accaaracracarcaaccaacrcccaarccaarcacarcacarcacaracaracaracaa ATAGICIGCCIACCCICAGGAAIATITITIGICIGIGGIACCICAGCCIAICATIGITIG AATGGCTCTTCAGAATCTATGTGCTTCCTCTTAGTGCCCCCTATGACCATCTAC ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCCACAAAAGAGTACCCATT ACTGAACAAGATTTATACAGTTATGTCATATCTAAGCCCCGCAACAAAAGAGTACCCATT CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC 36899 ACAACCTCTACTCAGTTCTACAAACTATCTCAAGAACTAAATGGGGACATGGAACGG CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA 37019 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTATTTTA GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA ATTCGAGATCGAATACAATGTAGAGCAGAGCTTCAAAACACCGAACGCTGGGGCCTC CTCAGCCAATGGATGCCCTGGGTTCTCCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT GAAGCTGTAAAACTACAAATGGAGCCCAAGATGCAGTCCAA 37359 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481 36719 36779 481 541 601 199 721 781 841 901 196 1021 1081 1141 1261 1321 1441 36359 36419 36539 36599 36659 36839 1201 37139 37199 37319 ઠે 셤 ò 셤 8 셤 ò 셤 à 硆 ò 엄 ઠ 셤 ઠે g ó g ò g g ò 셤 ò 용 ઠ 셤 8 6 6 6 ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting expression of human endogenous retrovirus envelope protein in cells of a tissue or culture, from its ability to induce syncytia.
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                                                                                                                                                                                                                                                                                                                                                                               Ruggieri
                                                                                                               Envelope protein; HERV; syncytia formation; placental development; syncytia; cancer; cell adhesion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2781 BP; 747 A; 770 C; 556 G; 708 T; 0 U; 0 Other;
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762. .2378
/*tag= a
/product= "envelope protein"
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Pred. No. 0;
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(INRM ) INST NAT SANTE & RECH MEDICALE.
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                      BP
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Best Local Similarity 93.7%;
Matches 1387; Conservative
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                      2781
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99FR-00011793
                                                                                                                                                       Human endogenous retrovirus
                                                                       entry)
                      DNA;
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                       AAF55630 standard;
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15-SEP-1999;
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                                           The present sequence represents an endogenetic retrovirus, which is associated with an autoimmune disease, and is integrated into the human genome. The retrovirus is human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. HERV-W nucleic acid fragments, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell proliferation in vitro
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                                                                                                                                                                                                                                 Sequence 7582 BP; 2156 A; 1876 C; 1538 G; 1796 T; 0 U; 216 Other;
                                                                                                                                                                                                                                                             89.4%; Score 1324.2; DB 3; Length 7582; 92.2%; Pred. No. 0; ive 24; Mismatches 92; Indels 0;
               Page 49-52; 53pp; French
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.23
Matches 1365; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Autoimmune disease; retrovirus; human endogenous retrovirus W; HERV-W; gag gene; pregnancy; multiple sclerosis; T cell proliferation; ss.
                                 CTCAGCCAATGGATGCCCTGGATTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATTG
                                                                                                 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATT
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/*tag= g
/note= "polypurine tract"
7256. .782
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/note= "U3-R of 3' LTR"
/563. .7569
                                                                                                                                                                                                                                                                                                                                                                      endogenous retrovirus W (HERV-W)
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/*tag= b
/note= "US of 5' LTR"
579. .596
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5581. .7194
/*tag= d
/note= "ORF1 env538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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7112. .7255
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/note= "R of
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                                                                                                                  Clone; human endogenous retrovirus; genome; autoimmune disease; multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes; disseminated lupus erythematosus; pregnancy; chromosomal marker; ss.
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ATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCTCAGCCTATCGTTGTTTG
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                                                                      Actigaacaacaatriatacagtratigicaratciaagccccccaaaaaaaagagtacccarr
                        AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC
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                                                                                                                                                           This sequence represents the complete sequence of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rhemmatoid polyarthritis, disseminated lupus erythematosus, insulin- dependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes associated with this susceptibility
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                                                             New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
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(pos:790. 752.aa:Phe) (pos:793. 792.aa:Phe) (pos:812. 814,aa:Lhr) (pos:812. 814,aa:Lhr) (pos:862. 864,aa:Tyr) (pos:865. 867,aa:Tyr) (pos:1174. 1116,aa:Arg) (pos:1174. 1116,aa:Arg) (pos:2017. 2019,aa:Leu) (pos:2017. 2019,aa:Lyr)

transl_except= (transl_except=
/*tag= b /product= "HERV-W

/*tag= a 763. 2379

.2019, aa:Lys) .2028, aa:Arg) .2046, aa:Arg) .2091, aa:Gln) .2172, aa:Asn)

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New human retrovirus HERV-W ENV proteins/peptides having superantigen activity useful for diagnosing and treating multiple sclerosis.
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                                                 AATGGCTCTTCAGAATCTATGTGCTTCCTCTTCTTAGTGCCCCCYATGRCCATCTAC
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99EP-00402690

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Human endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein; envelope protein; multiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective; antisense-therapy; autoimmune disorder; ds.
                                                                                             HERV-W envelope protein G encoding nucleic acid.
               AAH20069 standard; DNA; 2782
                                                                  (first entry)
                                                                  08-AUG-2001
                                         AAH20069
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RESULT 20

Location/Qualifiers 1. .762

Key 5'UTR

Human endogenous retrovirus

on the basis of the PBS t-RNA motif used for the classification of human endogenous retrovirus (HERNS) the full length endogenous provirus which was been located on the long arm of human chromosome 7 (7q21-22) has been designated HERN-W. The present invention describes proteins or peptides (I) having superantigen (SAg) activity comprising the ENV protein (ENV) of HERV-W, the surface protein (SU) and transmembrane (TW) sub-units. (I) have neuroprotective activity, and can be used in: vaccines; antisense-therapy; and HERN-W SAg activity-inhibitors. (I) and encoding DNA/RNA are useful for diagnosing multiple sclerosis (MS) or HERV-W-associated (Sisorders. (I) are also useful for identifying substances and optionally recovering) capable of binding to a retroviral superantigen associated with MS, substances capable of blocking stranscription or translation of HERV-W retroviral superantigen. A protein or peptide derived from (I), modified to be capable of blocking transcription or translation of HERV-W retroviral SAg is useful in therapy. Nucleic acid molecules encoding (I) are useful as vaccines against MS. Substances capable of blocking SAg activity, capable of binding to a retroviral capable of blocking SAg activity, capable of binding to a retroviral superantigen associated with MS, or capable of binding to a retroviral capable of blocking SAg activity, capable of binding to a retroviral superantigen of MS. (I) and nucleic acids encoding them are useful for the transment and considered with MS. The present sequence useful for the transming or preventing MS. Obtained using (I) are useful for the transment and considered with MS. The present sequence useful for the transment man and the man are useful for the transment man are useful for the transment man and moldered with man acids encodes the modeled of the man are useful for the transment man and moldered man are useful for the man useful for the man useful for the man useful for the man useful for the man useful for the man useful for the man useful for the man ö 9 Gaps ; 0 Score 1308.2; DB 5; Length 2782; Pred. No. 0; specifically claimed envelope protein of HERV-W designated G Sequence 2782 BP; 741 A; 768 C; 564 G; 709 T; 0 U; 0 Other; 0; Mismatches 108; Indels Claim 13; Fig 9; 94pp; English. 88.3%; Query Match
Best Local Similarity 92.7
Matches 1373; Conservative ò

1 ATGGCCCTCCCTTATCATACTTTTCTCTTTACTGTTCTCTTACCCCCTTTCGCTCTCACT

Db 1843 GTCGCCGACTCCCTGGTCACCTTGCAAGATC! Oy 1141 CAAAATCGAAGAGCTTTAGACTTGCTAACCGC Db 1903 CGAAATCGAAGAGCTTTAGTTAATCTAACCGG OY 1201 GGAGAAGAATCCTGTTATTATGTTAATCAATCAACGGAAGAATGCTGTTATTATGTTAATCAATC	RESULT 21 AAX25661 DAX25661; XX AC AAX25661; XX CAAX25661; XX Clone; human endogenous retrovirus; genomitiple sclerosis; rheumatoid polyarthm williple sclerosis; rheumatoid polyarthm williple sclerosis; rheumatosis; pregnax XX Clone; human endogenous retrovirus; genomitiple sclerosis; rheumatosis; pregnax XX Clone; human endogenous retrovirus. XX Clone; human	
	AGCACTCTAGACCCTAGAAGGACTAGATCTCTCAAAACTACATGAAACCCTCGGTACC GGCCCTAGCCCCTAGAAGGACTAGATCTCTCTCAAAACTACATGAAACCCTCGGTACC GGCCCTCTAGCCCCTAATTAATACCACCCTCAAACTACATGAAACCCTCGGTC CAAAACCCTACTAAACTTTGATTTAATACCACCCTCACTGGGCTCCATGAGGTCTCGGCC CAAAACCCTACTAAACTTTGATTTAATACCCCCTCACTGGGCTCCATGAGGTCTCGGCC CAAAACCCTACTAAACTTTGAATTTAATACCCCCCTGCACTTCGGCCATACTTTAATC CAAAACCCTACTAAACTTTGAATTTAATACCCCCTGCACTCGGCCATACTTTAATC CAAAACCCTACTAAACTTTGAATTTAATACCCCCCTGAAATTAATT	
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W; HERV-W;
                                                                                                                                           1843 GTCGCCGACTCCCCGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
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disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell proliferation in vitro
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                                                   ATAGECTACCCTCAGGAATATTTTTGTCTGTGGTACCTCAGCCTATCGTTGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTA
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                                                                                                                                                                       AATGGCTCTTCAGAATCTATGTGCTTCTTCTTAGTGCCCCCTATGACCATCTAC
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                                                                                                                                                                                                                        proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present DNA sequence was used in the exemplification of the invention.
                                                                                                     New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
   Wang J;
Wang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCACCCCTCCATGCCGCTGTATGACCAGTAGCTCCCCTTACCAAGAGTTTCTATGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                            87.7%; Score 1298.2; DB 10; Length 3464; 93.0%; Pred. No. 0; ive 0; Mismatches 98; Indels 6;
   Zhang J, Zhao QA
ou P, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                               Sequence 3464 BP; 1038 A; 913 C; 666 G; 845 T; 0 U; 2 Other;
 W, Ren F, Zhang
Weng G, Zhou P,
Boyle BJ;
                                                                                                                                                                       Disclosure; SEQ ID NO 2131; 1177pp; English
', Asundi V, Goodrich RW, I, Xue AJ, Wehrman T, Wen Wang D, Chen R, Xu C, Bo
                                                                                                                                                                                                            invention comprises the
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Best Local Similarity
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New polynucleotides, useful as hybridization probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA.
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                                                                                                       Example 2; SEQ ID NO 2085; 571pp; English
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            09-AUG-2002; 2002WO-US025485
                       09-AUG-2001; 2001US-0311261P
                                                 'n,
                                                            WPI; 2003-876918/81.
P-PSDB; ADF60170.
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The present invention describes isolated polynucleotide sequences (I), which encode polypeptides (II) with biological activity. Also described:

(I) a vector comprising (I); (2) an expression vector comprising (I); (3)

a host cell genetically engineered to comprise (I) which is operatively associated with a regulatory sequence that modulates expression of (I) in the host cell; (4) a polypeptide (II) encoded by (I); (5) a composition comprising the polypeptide of (4); (7) detecting (I) or the polypeptide of against the polypeptide of (4); (7) detecting (I) or the polypeptide of against the polypeptide of (4); (7) detecting (I) or the polypeptide of (4); (9) producing the polypeptide of (4); and (10) a collection of polymolectides comprising at least one of the polymucleotide sequences (I); The polymucleotides (I); and for generating antisense DNA or RNA. The polymore or primers, for chromosome or gene mapping, for the recombinant production of proceins, and for generating antisense DNA or RNA. The polymore contagnosmy of the polymucleotide sequence, which 1729 1909 1489 420 9 ACCITCACTGCCCACACATATGCCCCGCAACTGCTATAACTCTGCCACTTTGCATG AGCACCCTAGCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC 1610 ACCTTCACTGCCCACACCCATATGCCCCGCAACTGCTATCACTCTGCCACTCTTTGCATG CATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT GGAGCCACTGTCGTTGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGTGGAATT CAAGGTCAGGCAAGAAAAAAAGTAAAAGGAAGCAATCTCCCAACTGACCCGGGGACAT 1430 ATGGCCCTCCCTTATCATATTTTCTCTTTACTGTTCTTTTACCCTCTTTCACTCTCACT 1 AUGGCCCTTCCTTATCATACTTTTCTCTTTACTCTTTACCCCCTTTTCGCTCTCACT GCACCCCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA Gaps DB 10; Length 9502; Sequence 9502 BP; 2813 A; 2433 C; 1992 G; 2263 T; 0 U; 1 Other; . 9 98; Indels used in an example from the present invention ; Score 1298.2; ; Pred. No. 0; 0; Mismatches 1850 361 421 301

2689 1434 2869 1076 2509 1134 2569 1194 2629 1254 1314 GGCCTCCTCACCAATGGATGCCCTGGGTTCTCCCCTTATAGGACCTCTAGCAGCTCTA 1374 2389 1016 2269 2329 926 AAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGG ATATTGTTACTCCTCTTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCC CATICITICCTITITGITATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAG GTCCTTCAAAATCGAAGACTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTA TTTTAGGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTT AATGGCTCTTCAGAATCTATGTGCTTCCTCTTTCTTAGTGCCCCCTATGACCATCTAC ACTGAACAAGATTTATACAATCATGTC----GTACCTAAGCCCCACAAAAAAGAGTACC 2330 ACTGAACAATTTATACAGTTATGTCAATATCCTAAAGCCCCCGCAACAAAAGAGTACC ACAGGT - - CACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTA AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCCTCCCACACA CAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCAGGCCATACATTCAATC CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT AGAATTGAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 2690 1375 1077 2570 1195 2630 1255 1315 1435 2870 2270 1970 (2030 2090 2150 2210 781 841 901 957 721 601 661 481

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g ð a ABN97978 standard; DNA; 46340

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                                                        CAAGGTCAGGCAAGAGAAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACAT
                                                                                                                                                                                                           CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCCCTCCTTATCATATTTTCTCTTTACTGTTCTTTACCCCTTTTCACTCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1282; DB 3; Length 46340;
Pred. No. 0;
                                                                                                                                 chromosome 7q; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85; Indels
                                                                                                                                                                                                                                                                                                                                                                              RECH MEDICALE
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                                                                                                                                                                                                                                                                                                                                                                            (INRM ) INSERM INST NAT SANTE &
                                                                                          Human retroviral sequence HI3
                                                                                                                                 HERV-7q;
ds.
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92.3%;
                                                                                                                                                                                                                                                                                                     99WO-FR001513
                                                                                                                                                                                                                                                                                                                                         98FR-00007920
                                                                                                                                                                                      Human endogenous retrovirus
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Perin J,
                                                                                                                               disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-160587/14.
                                                                                                                                                  multiple sclerosis;
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Matches 1395; Conserv
                                                                                                                                                                                                                           WO9967395-A1
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                                                                                                                                   Autoimmune
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                                                                                                                  33294 ccircriginaaginigicrcriccagaarcaaagingiaaagciacaaarcgaricrica 33353
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CTTCTTAGGATCTCTAGCAGCTCTAATATTGATACTCCTCTTTGGACCCTGTATCTTTAA 33293
                                                             1469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequences of human endogenous retrovirus, HERV-7q, used diagnosis, treatment and prevention of autoimmune and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or other autoimmune diseases. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGCCCTCCCTTATCATACTTTTCCTCTTTACTGTTCTCTTACCCCCTTTCGCTCTCACT
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                                                          CCTCCTTGTTAAGTTTGTCTTTCCAGAATTGAAGCTGTAAAAGCTACAGATGGTCTTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HERV-7q; chromosome 7q; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INST NAT SANTE & RECH MEDICALE
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 134; 225pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perin J, Rieger F;
                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human retroviral sequence HE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.3%;
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                                                                                                                                                                                         AATGGAACCCCA 1481
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Best Local Similarity 92.1
Matches 1393; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Autoimmune disease;
multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-160587/14.
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                               Length 2784;
Seguence 2784 BP; 816 A; 755 C; 535 G; 678 T; 0 U; 0 Other;
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                             Score 1239; DB 3;
Pred. No. 0;
0; Mismatches 100;
                             Query Match
Best Local Similarity 91.0%;
Matches 1364; Conservative
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claim 25; SEQ ID NO 4541; 487pp; English
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                                                                                                                  n genome-derived single exon nucleic acid probes useful for analyzing expression in human cervical epithelial cells.
 AACAAAAGAGTACCCATTCTTTTTTTTTTGGAGCAGGAGTGCTAGGCGGAGTAGCT 1906
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26-MX-2000; 2000US-0201456P.
30-UJN-2000; 2000US-00608408
03-AUG-2000; 2000US-0234687P.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00234283.
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of siseases of the cervix. Intably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Itp.wipo.int/pub/published_pct_sequences
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Pred. No. 0;
0; Mismatches
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CTGGCATTGGCAGTATCACAACCTCTACTCAGTTCTACTACAAACTATCTCAAGAAATAA 1063
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0; Mismatches
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                        ACAAAAGAGTACCCATTCTTCCTTTTGTTATTGGAGCAGGAGTGCTAGGCGGAGTAGCTA
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                                                                                         TAGCAGCAGTAGTCCTTCAAATCGAAGACTTTAGACTTGCTAACCGCGGAAAGCGGGG
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                                             ATGGTGACATGGAACAGGTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCC
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gene expression in human fetal liver.
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2000US-0207456P.
2000US-00608408.
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human forcal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                              TATCTAAGGGAAACTCCACCTTCACTGCCCACACCCATATGCCCCGCAACTGCTATAACT
The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are use for antenatal diagnosis of human genetic disorders
                                                             Length 1894;
                                            Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
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                                                              DB 4;
                                                             Query Match 76.4%; Score 1131.6; Best Local Similarity 92.4%; Pred. No. 0; Matches 1218; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                        present invention relates to single exon nucleic acid probes (SENP)
                                                                   TAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGG
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053266.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
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885 ATGGTGACATGGAATGGGTCGCTGATACCCTGGTCACCTTGCAAGATCAACTTAACTCCC 944	4 TAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGG 1183	945 TAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACCGCGGAAAGCGGGG 1004	4 GAACCTGTTTATTTTAGGAGAAGAACGCTGTTATTATGTTAATCAATC		4 CTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCGAGGAGGAGCTTCAAAACA 1303	S CCGAGAAAGTTAAAGAAATTCAAGGTCGAATATAACGTAGAGCAAAGGAGCTGCAAAACA 1124	4 CGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTC 1363	S CTGGACCCTGGGGCCTCCTCAGCCAATGGATGCCCTGGATTCTCCCCCTTCTTAGGACCTC 1184	4 TAGCAGCTCTAATATTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGT 1423	TAGCAGCTATAATATTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGT 1244	4 TIGICITCTACCAGAATTGAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481	S TIGICITITICCAGAAICGAAGCAGTAAAACTACAAATCGTICTICAAAIGGAGCCCCA 1302	
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Search completed: January 22, 2005, 16:40:33 Job time : 695.669 secs

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                                                                             ; Search time 137.138 Seconds (without alignments) 7676.074 Million cell updates/sec
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/cgm2_6/ptodata/1/ina/RECTUS_COMB.seq:*
/cgm2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-175-928-3
US-08-979-8478-108
US-08-68-68-88-18
US-08-721-499-2
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Maximum Match 100%
Listing first 45 summaries
                                                     nucleic search, using sw model
                                                                              2005, 12:03:14
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Maximum DB
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
THERAPEUTIC PURPOSES
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Sequence 3
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MEDIUM TYPE: Floppy disk
COMPUTER: IND PC Compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INPORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-836-6400
                                 US-08-716-351A-5
US-08-258-420-9
US-08-258-420-9
US-08-850-961-13
US-09-479-776-13
US-09-315-127-10
US-09-011-745-7
US-09-011-745-7
US-09-651-858-3
US-09-621-976-14048
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US-08-709-209-310
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SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-08-979-8478-105
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                                                                                                                                                                                                                                                                                                                                                                                                 PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
                                                                                                                                                                                                                                                                                                                                                                                                                         COLETTE
                                                                                                                                                                                                                                                                                                                     Sequence 105, Application US/08979847B Patent No. 6582703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRI
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22330
                                                                                                                                                                                                                                                                                                                                                                                                                                       MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 base pairs
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PERRON, HERVE
BESEME, FREDERIC
BEDIN, PREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 210
          8060
10910
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INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
THERAPEUTIC PURPOSES
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                                          ATTCGAGATCGAATACAACGTAGAGCAGAGGAGCTTCGAAACACTGGACCCTGGGGCCTC
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                   ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAAACACCGAAACGCTGGGGCCTC
                                                                                                    CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTTTAGGACCTCTAGCAGCTCTAATATTG
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COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IMP FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 20.4%; Score 302; DB 4; Best Local Similarity 92.7%; Pred. No. 1.1e-87; Matches 317; Conservative 0; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 108, Application US/08979847B Patent No. 6582703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOLIVET-REYNAUD, C
MANDRAND, BERNARD
GARSON, JEREMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 1329 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PERRON, HERVE
BESEME, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
ULE TYPE: cDNA
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US-08-979-847B-108
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                                                              ACCTTCACTGCCCACACCCATATGCCCCGCAACTGCTATCACTCTCGCCACCTTTGCATG
                                                                                                                                           1168 CATGCAAATACTCATTATTGGACAGGAAAAATGATTAATCCTAGTTGTCCTGGAGGACTT
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ATGCAGCGTCCCGGAAATATTGATGCCCCATCGTATAGGAGTCTTTCTAAGGGAACCCCC
                                                                                                                                                                                                     GGAGCCACTGTCTTGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGGTGGAATT
                                                                                                                                                                                                                                                                                                                               1288 CAAGATCAGGCAAGAGAAAACATGTAAAAGAAGTAATCTCCCAACTCACCCGGGTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCCACTTCCGTTTTAGTA
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                                                                                                                       CATGCAAATACTCATTATTGGACAGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT
                                                                                                                                                                                                                                                                                        CAAGGTCAGGCAAGAAAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT
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61 GCACCCCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120
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APPLICANT: Merberg, David
APPLICANT: Treacy, Maurica
APPLICANT: Treacy, Maurica
APPLICANT: Spaniding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
91.5%; Pred. No. 3.5e-46;
tive 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/721,489
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Pred. No. 3.5e-46;
0; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                    522 ACCTTCACTGCCCACACCCAT 542
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08721489
Patent No. 5786465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 496-851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOy, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.7%;
Best Local Similarity 91.5%;
Matches 184; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
  Best Local Similarity 91.5
Matches 184; Conservative
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STATE: Massachusetts
COUNTRY: U.S.A.
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US-08-721-489-2
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US-08-721-489-2
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       1140 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTT 1199
                                                                                                  1200 AGGAGAAGGATGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGA 1259
                                                                                                                                                                                                                                            121 AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCTTGGGGGCCT 180
                                                                                                                                                                                                                                                                                                                   181 CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTTTAGGACCTCTAGCAGCTATAATAATATT 240
                                                                                                                                            61 AGGGGAAGAATGCTGTTAGTATCTTAATCATCTGGAATCATTACTGAGAAAGTTAAAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TTTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTCCAGAAT 300
                                                      9
                                  1 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGGAACCTGTTTATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Treacy, David
APPLICANT: Treacy, David
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SCREETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genefice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts COUMTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 48, Application US/08686878A Patent No. 5708157
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BROWN, SCOCE A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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401 Length 542; Indels

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VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
THERAPEUTIC PURPOSES
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                                                                                                                                                                          1300 AACACCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGA 1359
1060 ATAAATGGTGACATGGAACAGGTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAAC 1119
                                                                                                                              526 TCTTTGGCAGCAATGACTCTCCAAAACCGCCGAGGCCCACACCTCCTCACTGCTGAGAAA 585
                                                                                                                                                                                                                                                                                                                                                                                             706 AACTCTTATACCAA-----CCTCTGGAGTTGGGCAACATGGCTTCTTCCATTTCTAGGT 759
                                         466 TICTCAGACAGTTTGCAAGAAATAATGAAATCTATTCTTACTTTACAATCCCAATTAGAC 525
                                                                                                                                                                                                                     586 GGAGGACTCTGCACCTTCTTAGGGGAAGAGTGTTTTTTTACACTAACCAGTCAGGGATA 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       760 CCCATGGCAGCCATCTTGCTGTTACTCACCTTTTGGGCCCTGTATTTTTAAGCTTCTTGTC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              820 AAATTTGTTTCCTCTAGGATCGAAGCCATCAAGCTACAGATGGTCTTACAAATGGAACCC 879
                                                                                     TCCCTAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGA
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700 South Washington Street, Suite 300
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PRICHARD AND BATA:
APPLICATION NUMBER: US/08/691,563
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFRENCE/DOCKET NUMBER: WPB 38588
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Herve PERRON
APPLICANT: Frederic BESEME
APPLICANT: Frederic BESEME
APPLICANT: Glaucia PARAHOS-BACCALA
APPLICANT: Glaucia PARAHOS-BACCALA
APPLICANT: Glaucia PARAHOS-BACCALA
APPLICANT: Colette JOLINET
APPLICANT: Bernard MANDRAND
TITLE OF INVENTION: VIRAL MATERIAL AND
TITLE OF INVENTION: ASSOCIATED WITH MU
TITLE OF INVENTION: THERAPEUTIC PURPOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,766
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Patent No. 6579526
GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & B
STREET: 700 South Wa
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: U.S.A.
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000 GGTACTGGCATTGGCAGTATCACAACCTCTACTCAGTTCTACTACAAACTATGTCTCAAGAA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 CAGTGCAGAGCCATACAACTATATCCCTATTTATAGGGTTAGGAATGGCTACTGCTACA 405
                    GCACCCCTCCATGCTGCTGTACAACCAGTAGCTCCCTTACCAAGAGTTTCTATGAAGA 120
                                         121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC 180
                                                                                                                                         ATGCAGCGTCCCGGAAATATTGATGCCCCATCGTATAGGAGTCTTTCTAAGGGAACCCCC 521
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Pred. No. 1.1e-36;
0; Mismatches 234; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTHE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563C
FILING DATE: 02-AUG-1996
ATTORNEY/AGRNT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-6400
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700 South Washington Street, Suite 300
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Colette JOLIVET
Bernard MANDRAND
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                                                                                                                                                                                                                                                                                                                                                 ; Sequence 58, Application US/08691563C
; Patent No. 6001987
; PAREAL INFORMATION:
; APPLICANT: Herve PERRON
                                                                                                                                                                                              ACCTTCACTGCCCACACCCAT 201
                                                                                                                                                                                                                                        ACCTICACTGCCCACACCCAT 542
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Frederic BEDIN
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Best Local Similarity 55.7
Matches 302; Conservative
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
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ZIP: 22314
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US-08-691-563C-58
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STATE:
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9.8%; Score 145.6; DB 4; Length 1722;
Best Local Similarity 55.7%; Pred. No. 1.1e-36;
Matches 302; Conservative 0; Mismatches 234; Indels 6;
                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION WINDOWN>
ATTORNEY AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET WINDER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEPAX: 703-836-6787
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-08-979-8478-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1722 base pairs
                         ADDRESSEE: OLIFF & BER:
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
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COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                 USA
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TUKE, PHILIP
TUKE, PHILIP
TUKENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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                                                                                                                                                                                                                                                                                                            Length 1722;
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                                                                                                                                                                                                                                                                                                            Score 145.6; DB 4;
Pred. No. 1.1e-36;
0; Mismatches 234;
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BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
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Patent No. 6582703
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
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MANDRAND, BERNARD
GARSON, JEREMY
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                                                                                                                                                                                                                                                                                                               9.8%;
                                     INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1722 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-374-766-58
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 55.7
Matches 302; Conservative
               703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA 1481
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US-08-979-847B-54
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VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACTI
THERAPEUTIC PURPOSES
                                                                                                              TGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTTGTCTCTTCCAGAA 1438
                                        1805 GAACTTGGAAATGGTTCTTGGGTTCTTCCCCTTACAGGCCCACTTGTTAGTCTCCTAC 1864
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                                                                                                                                                                                   1865 TTTTGCTCCTTTTTGGTCCATGTCTCCTAAATCTAATAACCCAATTTGTCTCCTCTCGCC 1924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Oliff & Berridge
700 South Washington Street, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 131.2; DB 3;
Pred. No. 5.6e-32;
0; Mismatches 183;
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FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: BETINGE, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38588
TELECHOUNICATION INFORMATION:
TELECHONE: 703-836-6400
TELEFAX: 703-836-2787
                                                                                                                                                                                                                                                                                                                        1925 Trcaggccaraaagcrccagacg 1947
                                                                                                                                                                                                                                                         1439 TIGAAGCTGTAAAGCTACAGATG 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fredeil APPLICANT: Glaucia PARANHOS-BALLANT: Glaucia PARANHOS-BALLANT: Florence KOMURIAN-PRADEL APPLICANT: Colette JOLIVET COLOTTE Bernard MANDRAND COLOTTE BERNARD MANDRAND COLOTTE BERNARD MATERIAL CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 46, Application US/08691563C Patent No. 6001987 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 57.6%;
Matches 257; Conservative C
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Frederic BESEME
Frederic BEDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1859 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid strandEdNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22314
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bernard MITILE OF INVENTION: VITLE OF INVENTION: VITLE OF INVENTION: STATES OF INVENTION: STATES OF INVENTION: STATES OF INVENTION: STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCGAGATCGAATACAATGT---AGAGCAGAGCTTCAAAACACCCGAACGCTGGGGCC 1318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_Ft_genes Version 2.0
SEQ ID NO 249
                                                                                                                                                                                                                                              Sequence 249, Application US/09799451
Patent No. 6783969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang, Jian-Rui
Ma, Yunging
Yamazaki, Victoria
Chen, Rui-hong
                                                                                                                                                                                                                                                                                                                                              Tang, Y. Tom
Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
Ren, Feiyan
Zhang, Jie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhiwei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wehrman, Tom
Ghosh, Reena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (382)..(1995)
US-09-799-451-249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 803
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1505
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       1480
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TUKE, PHILIP
INVENTION: VIRAL MATERIAL AND NUCLECTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
                                                                                                                            1036 ITCTACTACAAACTATCTCAAGAAATAAAAAGGTGACATGGAACAGGTCACTGACTCCCTG 1095
                                                                                                                                                                                                                                                               1096 GICACCTIGCAAGAICAACTIAACICCCIAGCAGCAGIAGICCTICAAAAICGAAGAGCI 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1216 TATTATGTTAATCAATTCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATA 1275
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

SOFTWARR: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

RPLICATION NUMBER: US/08/979,847B

FILING DATE: 26-NO. 6582703-1997

CLASSIFICATION: CURROWN>
Score 131.2; DB 4; Length
Pred. No. 5.6e-32;
0; Mismatches 183; Indels
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PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1456 CAGATGGTCTTACAAATGGAACCCCA 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-979-847B-42; Sequence 42, Application US/08979847B; Sequence 42, Application US/08979847B; Patent No. 6582703; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOLIVET-REYNAUD, C
MANDRAND, BERNARD
GARSON, JEREMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FREDERIC
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ADDRESSEE: OLIFF & BERN
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210
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      8.9%;
al Similarity 57.6%;
257; Conservative
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             Query Match
                                                   Local
                                                   Best Loca
Matches
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APPLICANT: Frederic BESEME
APPLICANT: Frederic BEDIA
APPLICANT: Frederic BEDIA
APPLICANT: Colette JOLIVET
APPLICANT: Colette JOLIVET
APPLICANT: Colette JOLIVET
APPLICANT: Bernard MANDRAND
APPLICANT: Bernard MANDRAND
APPLICANT: BERNARD MANDRAND
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: THERAPEUTIC PURPOSES
AUTHENTION: THERAPEUTIC PURPOSES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
                                                                                                                                                                                                                                                                                                                                                  1336 CCCIGGGIICICCCCTICITAGGACCICTAGCAGCICTAAIAITGIIACICCICTITGGA 1395
                                                                                      1216 TATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATA 1275
                                                                                                                                                                                                                  1276 CAATGTAGAGCAGGAGCTTCAAAACACGGAACGCTGGGGGCCTCCTCAGCCAATGGATG 1335
                                                                                                                                                                                                                                                                                1332 TCTGAAATCAGACAACGCCTTTCAAATTC-----CTATACCAACCTCGGAGTTGGGCA 1385
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                 1212 CTAGACCTCCTCACTGCTGAGAAGGAGGACTCTGCACCTTCTTAAGGGAAGAGTGTTGT 1271
                                                                                                                                                1272 CITITACACIAACCAGICAGGGAIAGIAIGAGAIGCIGCCGGCAITIACAGAAAAAGGCI 1331
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,766
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700 South Washington Street, Suite 300
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PRICHARD AND BATA:
APPLICATION NUMBER: US/08/691,563
FILING DATE: 02-AUG-196
ATOMNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFRENCE/DOCKET NUMBER: WPB 38588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGATGGTCTTACAAATGGAACCCCA 1481
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STRANDEDNESS: single
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: U.S.A.
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GENERAL INFORMATION:
APPLICANT: Herve E
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COUNTRY: U.S
ZIP: 22314
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APPLICANT: NAZERIAN, KEYVAN
APPLICANT: CALVERT, JAY G.
APPLICANT: CALVERT, JAY G.
APPLICANT: WITTER, RICHARD L.
APPLICANT: WANAGIDA, NOBORD
TITLE OF INVENTION: VACCINE COMPRISING FOWLPOX VIRUS
TITLE OF INVENTION: RECOMBINANTS EXPRESSING THE ENVELOPE GLYCOPROTEIN OF AN
TITLE OF INVENTION: ANIAN RETICULOENDOTHELIOSIS RETROVIRUS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: primer_bind
LOCATION: 346.366
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer bind
LOCATION: 801.821
OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                    LOCATION: 484.502
OTHER INFORMATION: 12-5-158.misl
NAME/KEY: miselbinding
LOCATION: 504.523
OTHER INFORMATION: 12-5-158.mis2, potential complement
                                                                                                                                                                                                                               or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.8%; Score 130.2; DB 4; Best Local Similarity 67.6%; Pred. No. 8e-32; Matches 211; Conservative 0; Mismatches 99;
                                                                                                                                                                                                       LOCATION: 503
OTHER INFORMATION: 12-5-158 : polymorphic base C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc binding
LOCATION: 491.515
OTHER INFORMATION: 12-5-158 potential probe
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; Patent No. 5403582
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: 314, 336, 793
OTHER INFORMATION: n=a, g, c or t
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                                                                                                                            ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
                                                                                                                                                                                                                                                         NAME/KEY: misc_binding
LOCATION: 484..502
  NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
SEQ ID NO 406
LENGTH: 1001
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APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Bougueleret, Lydie
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REPERENCE: 62.043.CIP
CURRENT APPLICATION NUMBER: 2000-09-27
RRIOR APPLICATION NUMBER: US 99/536,178
PRIOR PLILNG DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1036 TTCTACTACAAACTATCTCAAGAAATAAATGGTGACATGGAACAGGTCACTGACTCCCTG 1095
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                                                                                                                                                                                                                                                                                                                                                                                      Score 131.2; DB 4; Length Pred. No. 5.6e-32; 0; Mismatches 183; Indels
                             : WPB 39046A
                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1456 CAGATGGTCTTACAAATGGAACCCCA 1481
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEPAK: 703-836-2787
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1859 base pairs
REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 406, Application US/09671317
Patent No. 6528260
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.6%;
Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-09-671-317-406
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Sequence 4, Application US/09078294
Patent No. 6265211
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Best Local Similarity 55.7%;
Matches 263; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 80246
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                                                                                                US-09-078-294-4
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,282B
FILING DATE: 19930121
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY UR., GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1644-104P
TELEPHONIS: 703-205-8000
TELEPHONIS: 703-205-8050
SEE: BIRCH, STEWART, KOLASCH & BIRCH: 8110 Gatehouse Road Suite 500 East Falls Church
                                                                                                                                                                           ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Matches 268, Conservative
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STRANDEDNESS: double
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US-08-007-282B-1
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                                                                                                                                                  COUNTRY:
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Best Local 8
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GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Cancilla, Michael R.
TILLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILLE REPERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
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Pred. No. 1.3e-25;
0; Mismatches 202;
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; APPLICANT: Collins, Mary KL
; APPLICANT: Collins, Mary KL
; APPLICANT: Cosset, Francois-Loi
; APPLICANT: Cosset, Francois-Loi
; TILE OF INVENTION: Expression systems; FILE REFERENCE: 09/011,745
; CURRENT APPLICATION NUMBER: US/09/011,745
; CURRENT FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: PCT/GB96/02061
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us-09-319-156b-9.rni

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2692 AAATTATCCCATCAGTTAATATCTGATGTCCAAGTCTTATCCGGTACCATACAAGATTTA 2751
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US-09-555-352-1
Sequence 1, Application US/0955352
Patent No. 6544779
GENERAL INFORMATION:
    OTHER INFORMATION: construct
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OTHER INFORMATION: n is
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LOCATION: (3612)
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LOCATION: (3613)
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LOCATION: (3802)
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LOCATION: (3799)
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LOCATION: (3800)
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Best Local S
Matches 224
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                                                                                                                                                                                                                                                                                                                                                          Length 2518;
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                                                                                                                                                                                                                                                                                                                                                     Score 114.2; DB 3; Length
Pred. No. 2.3e-26;
0; Mismatches 183; Indels
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APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
TITLE OF INVENTION: Expression systems
FILE REPERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                   OTHER INFORMATION: n is any nucleotide
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Patent No. 6165715
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 55.0
Matches 224; Conservative
                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)
                                                                                                                                                                 TYPE: DNA
ORGANISM: RD114
                                                                                                                                           LENGTH: 2518
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US-09-011-745-8
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                                                                                                                                                                                                                                                                                                                                                        Query Match
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Pred. No. 8.6e-24;
0; Mismatches 186; Indels 3;
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Patent No. 6566325
GENERAL INFORMATION:
APICLARY: ROSEN et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: P203221
CURRENT PAPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
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Best Local Similarity 55.0%;
Matches 231; Conservative (
                                               Yang, Yonghong
Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1936)..(2364)
US-09-620-312D-171
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ORGANISM: Homo sapiens
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US-09-904-615-12
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51.5%; Pred. No. 1.5e-25;
tive 0; Mismatches 243; Indels 0;
APPLICANT: Cichutek, Klaus
APPLICANT: Merget-Millitzer, Heike
TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH
TITLE OF INVENTION: MODIFIABLE SURFACE CAPSID PROTEINS
FILE REFERENCE: 11692-005001
CURRENT APPLICATION NUMBER: US/09/555,352
CURRENT APPLICATION NUMBER: PS/09/555,352
CURRENT FILING DATE: 2000-08-24
PRIOR PILING DATE: 1998-11-27
PRIOR FILING DATE: 1998-11-27
PRIOR FILING DATE: 1998-11-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
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CRGANISM: Murine leukemia virus
US-09-555-352-1
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
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Best Local Similarity 51.5
Matches 258; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
LENGTH: 4776
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3; Gaps

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APPLICANT: YOON, JI-WON
APPLICANT: JUN, HEE-SOOK
APPLICANT: JUN, HEE-SOOK
APPLICANT: ARN, JONG-SEONG
APPLICANT: ARN, JONG-SEONG
APPLICANT: HA, YOUNG-JU
APPLICANT: CHUNG. SEONIL
APPLICANT: CHUNG. SOO-IL
APPLICANT: CHUNG. SOO-IL
APPLICANT: CHUNG. SOO-IL
APPLICANT: CHUNG. SOO-IL
APPLICANT: CHUNG. SOO-IL
APPLICANT: ON WHER: US/09/120,653D
CURRENT APPLICATION NUMBER: US/09/120,653D
FRIOR APPLICATION NUMBER: KR 98-10108
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: KOPACHIN 1.71
                                                                                                                                                                                                                                                                                 59089 TGACAGCCATCTTGCTAATAGTCGCATTTGGGCCCTGTATTTTTAACCTCTTGGTCAAAT 59148
                                                                                     58917 --ATTCTGCACTTCTTAGGGGTAGAGTGTTGTTTTTATACTAACCAGTCAGGGATAGTAT 58974
                                                                                                                                          1244 CTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGGTTCAAAACA 1303
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                                                                                                                                                                                         58975 GAGATACCACCCAGTGTTTACAGGAAAAGGCTTCTGAAATCAGACAATGCCTTTCAAACT
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Best Local Similarity 55.5%; Pred. No. 1.3e-18;
Matches 218; Conservative 0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: DIABETES-SPECIFIC RETROVIRUS ENDOGENOUS ERV-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 6, Application US/09120653D; Patent No. 6365727
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                                                                                                                                                                                                                                                                                                                                                         Length 2342;
                                                                                                                                                                                                                                                                                                                                                       7.1%; Score 104.8; DB 4; Length 54.8%; Pred. No. 2.5e-23; ive 0; Mismatches 187; Indels
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; Sequence 3, Application US/09078294
; Patent No. 6265211
; GENERAL INFORMATION:
    APPLICANT: Choo, Kong-Hong Andy
    APPLICANT: Choo, Kong-Hong Andy
    APPLICANT: Cancilla, Michael R.
    TITLE OF INVENTON: A NOVEL NUCLEIC ACID MOLECULE
    FILE REFERENCE: Davies Col
    CURRENT APPLICATION NUMBER: US/09/078,294
    CURRENT FILING DATE: 1998-05-13
    NUMBER OF SEQ ID NOS: 29
    SOFTWARE: PatentIn Ver. 2.0

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PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR PILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR FILING DATE: 1998-08-31
NUMBER: OF SEQ ID NOS: 170
SOFTWARE: PALENTIN Ver. 2.0
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Matches 206; Conservative
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                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-615-12
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Best Local Similarity
Matches 230; Conserv
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LENGTH: 80595
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US-09-078-294-3
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1134 AGTCCTTCAAAATCGAAGAGCTTTAAGACTTGCTAACGGCCCAAAAGAGGGGGAACCTGTTT 1193
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US-09-513-999C-24228

Sequence 24228, Application US/09513999C

Patent No. 6783961

APPLICANT: Dundlert, A.

APPLICANT: Duclert, A.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2002;
                                                                                                                                                                                                                                                                                                                                                                                                                        44.7%; Score 70.2; DB 4; Length 2 48.7%; Pred. No. 4.2e-12; ive 0; Mismatches 233; Indels
                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: 5, retroviral vector
FILE REFERENCE: 44137-5023, U. of Tennessee CURRENT APPLICATION NUMBER: US/09/315,127; CURRENT FILING DATE: 1999-05-20; NUMBER OF SEQ ID NOS: 23; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 7; LENGTH: 2002

TYPE: DNA
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NAME/KEY: CDS

LOCATION: (65)..(1999)

US-09-315-127-7
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              APPLICANT: JUN, HEB-SOOK
APPLICANT: PARK, HAB-JOON
APPLICANT: PARK, HAB-JOON
APPLICANT: AHN, JONG-SEONG
APPLICANT: AHN, JONG-SEONG
APPLICANT: AHN, YOUNG-JU
APPLICANT: CHUNG, SOO-IL
TITLE OF INVENTION: DNA and peptides of a diabetes-specific endogenous retrovirus
FILE REFERENCE: 98-338
CURRENT APPLICATION NUMBER: US/09/120,653D
CURRENT APPLICATION NUMBER: KR 98-10108
PRIOR FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 33
SOURBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3126 grececcaacarcectricicaccirroracercecereceaaccarcerregieniacres 3185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTOTTOTTTGACACTAACCAGGCACGGATAGCATGAGAT------GGCACCCAGC 3065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1388 TCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATTGAAGCTG 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3186 certricececeacarrrrraacerrerrereaarrrer-rrereragarresageer 3244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1148 GAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTAGGAGAAG 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1208 AACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAG 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1268 ATCGAATACAATGTAGAGCAGGAGCTTCAAAACACCGAACGCTGGGGCCTCCTCAGCC 1327
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          329 CCTTTGGGCCCAGCATTTTTAACGTTCTTGTCAAATTTGT-TTGTCTAGATTCGAGGCCT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2895 AATCTGTCCTTACTTTACAATCCAAAATAGACACTTTGGCAGCAGTGACTCGCCAAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGAGGCATAGATGTCCTCACTGCTGAAGAAGAGACTCTGCACTTTCTTAGGGGAAG
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Sequence 7. Application US/09315127

Patent No. 6448390

GENERAL INFORMATION:

APPLICANT: THE University of Tennessee, c/o Richard Cox

ITTLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and

TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 4.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: DIABETES-SPECIFIC ENDOGENOUS RETROVIRUS ERV-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1448 TAAAGCTACAGATGGTCTTACAAATGGAACCCC 1480
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                                                                1448 TAAAGCTACAGATGGTCTTACAAATGGAACCCC 1480
                                                                                                         388 rchagcrachgarderchrachrandadccc 420
                                                                                                                                                                                                                                    Sequence 1, Application US/09120653D Patent No. 6365727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.5%;
Matches 218; Conservative (
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: YOON, JI-WON
APPLICANT: JUN, HEE-SOOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-120-653D-1
                                                                                                                                                                                           RESULT 23
US-09-120-653D-1
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US-09-315-127-7
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US-08-979-847B-102
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                                                                                                                                                                                                                                                                                                                                                                                                                   CICTGIAICTITAACCTCCTTGITAAGTTTGICTCTTCCAGAATCAAAGCTATAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Portion of
OTHER INFORMATION: construct
                                                                                                                                                                                                                                                                                                                            Length 149;
                                                                                                                                                                                                                                                                                                                                         9.6e-13;
                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COLLINS, MARY KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT PILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER APPLICATION NUMBER: G89517263.1
EARLIER PILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN OFF. 2.0
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1456 CAGATGGTCTTACAAATGGAACCCCA 1481
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Pred. No. 9
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Patent No. 6165715
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                O
                                                                                                                                                                                                                                                         LOCATION: 135 7

COTHER INFORMATION: m=a or C

US-09-513-999C-24228
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 24228
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Best Local Similarity 88.4
Matches 76; Conservative
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OTHER INFORMATION: n is
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LOCATION: (3911)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
                                                                                                                                                                                            LOCATION: 129 OTHER INFORMATION: n=a,
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                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                             NAME/KEY: misc_feature
LOCATION: 127
                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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US-09-011-745-9
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                                                                                                                                                               FEATURE:
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MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILLIP
INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1314 GGGCCTCCT------CAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGG 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1134 AGTCCTTCAAAATCGAAGGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTT 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1254 TAAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTG 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3189 GGCCAAACTAAGGGAAAGGCTTAATCAGAGACAAAAACTATTTGAGTCAGGCCAAGGTTG 3247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3248 GTTCGAAGGGCAGTTTAATAGATCCCCCTGGTTTACCACCTTAATCTCCACCATCATGGG 3307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1359 ACCICTAGCAGCICTAAIATIGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGT 1418
                                                                                                                                                                                                                            3308 ACCICIAAIAGIACICIIACIGAICIIACICIIIGGACCCIGCAIICICAAICGAIIAGI 3367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3128 AGCCCTAAAAGAAGAATGTTGTTTTTTATGCAGACCACGGGACTAGTGAGAGAACAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1074 GGAACAGGTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                           3008 caacgaagicgaaaarcaarraccaaccragaaagrcacrgaccrcgrrgrcrdaagr
                                                                                                                                                                     15;
                                                                                                     Score 70; DB 3; Length 3925;
Pred. No. 7.5e-12;
                                                                                                                                                                  0; Mismatches 215; Indels
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COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1419 TAAGTTTGTCTTCCAGAATTGAAGCTGTAAAG 1452
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APPLICATION NUMBER: US/08/979,847B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE

; LOCATION: (3913)
; OTHER INFORMATION: n is any nucleotide
US-09-011-745-9

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BESEME, FREDERIC
BEDIN, FREDERIC
                                                                                                              4.7%;
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COMPUTER READABLE FORM:
                                                                                                        Query Match
Best Local Similarity 49.3°
Matches 224; Conservative
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RESULT 29
US-08-766-528-1
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                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
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                            ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WFB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-2787
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REPERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1996-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
BARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
DATE: 26-No. 6582703-1997
                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGATGGTCTTACAAATGGAACCCCA 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAATTGTTCTTCAAATGGAGCACCA 86
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OTHER INFORMATION: n is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (3774)
OTHER INFORMATION: n is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-011-745-5
Sequence 5, Application US/09011745
Patent No. 6165115
GENERAL INPORMATION:
                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: n is
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NAME/KEY: misc feature
-----TON: (3774)
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SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                        US-08-979-847B-102
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OTHER IN
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1030 ACTCAGTTCTACTACAAACTATCTCAAGAAATAAATGGTGACATGGAACAGGTCACTGAC 1089
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4.6%; Score 68.4; DB 3; Length 6028;
Best Local Similarity 49.5%; Pred. No. 3.2e-11;
Matches 217; Conservative 0; Mismatches 206; Indels 15.
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                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (3963)
OTHER INFORMATION: n is any nucleotide
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INFORMATION: n is any nucleotide
                                                             FEATURE:
NAME/KRY: misc_feature
LOCATION: (3962)
OTHER_INFORMATION: n is any nucleotide
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NAME/KEY: misc feature
LOCATION: (3964)
OTHER INFORMATION: n is any nucleotide
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Patent No. 6190861
GENERAL INPORMATION:
TITLE OF INVENTION: MOLECULAR SEQUITILE OF INVENTION: AND METHODS OF NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LISTRET: 60 State Street
CITY: Boston
STREET: Massachusetts
COUNTRY: USA
COMPUTER READABLE FORM:
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Sequence 1, Application US/09661858
Patent No. 6699663
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%; Score 68.4; DB 3; Length 8060; 53.3%; Pred. No. 3.9e-11;
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ZIP: 02.09
ZIP: 02.09
ZOMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-038CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (61)227-7400
                                                                                                                    APPLICATION NUMBER: US/08/766,526
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 8060 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                         FILING DATE:
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US-09-661-858-1
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1104
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Pred. No. 3.9e-11;
0; Mismatches 126; Indels
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                                                                                                                                                                                                            REGISTRATION NUMBER: 35,965
REPERBUCE/DOCKET NUMBER: MGP-038CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/09/661,858 FILING DATE: 14-Sep-2000 PRIOR APPLICATION DATA:
                                                                                        APPLICATION NUMBER: 08/766,528 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                     LERGTH: 8060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     completed: January 22, 2005, 19:36:59
                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Louis Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.3%;
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 141.138 secs
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us-09-319-156b-9.rnpb

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Sequence 105, App
Sequence 18, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
                                                                                                                                                                           January 22, 2005, 12:12:40 ; Search time 804.34 Seconds (without alignments) 10579.682 Million cell updates/sec
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19: \cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-016-249-3
US-10-13-036-3
US-09-854-867-21
US-09-873-367C-81
US-10-632-393-30
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6 US-10-637-565-18
6 US-10-416-642-4
US-09-902-535-1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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13306.6 88.2 11306.6 11306.6 188.2 11116.4 75.4 11116.4 75.4 1116.4 75.4 1116.4 75.4 1116.4 75.4 116.6 83.9 82.8 39.4 825.5 377.8 25.5 377.8 25.5 377.8 25.5 377.8 25.5 377.8 25.5 377.8 25.5 377.8 25.5 377.8 25.5 377.8 25.5 377.8 25.5 377.8 25.5 23.8 35.3 23.8 35.3 23.8 35.3 23.8 25.5 25.6 20.0 22.9 6 15.5 22.9 6 15.8 11.7 7 11.7	16 US-10-632-793-2	13 US-10-087-192-73	9 US-09-864-761-444	16 US-10-632-793-24	9 US-09-864-761-21	16 US-10-363-616				L3 US-10-027-632-32	L3 US-10-027-632	LS US-10-027-632	L5 US-10-027-632-3224	L5 US-10-029-386	L3 US-10-027-632	l3 US-10-027-632-322575	LS US-10-027-632	15 US-10-027-632-32257	LS US-10-292-798-13	3 US-08-979-847-108	15 US-10-114-104-108) US-09-864-761-	13 US-10-027-632-31641	LS US-10-027-632	13 US-10-027-632-8654	IS US-10-027-632-8654	US-09-864-761-7501	L5 US-10-029-386-2025	US-09-864-761-7310	13 US-10-027-632-15008	15 US-10-027-632-15008		
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA.
THERAPEUTIC PURPOSES
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                                    ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACAAAAAAAGATACCCATT
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                         AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC
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KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
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; Sequence 105. Application US/10114104
; Publication No. US20030198647A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OLIFF & BERRI STREET: P.O. BOX 19928 CITY: ALEXANDRIA STATE: VA COUNTRY: USA ZIP: 22320 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PERRON, HERVE
BESEME, FREDERIC
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100.0%; Score 1481;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1481; Conservative 0; Mismatches
                                 39046A
       REGISTRATION WINDER: 30,024
REGISTRATION WHOBER: 30,024
REFERENCE/DOCKET NUMBER: 40,024
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-836-6400
TELECHAX: 703-836-787
INFORMATION FOR SEQ ID NO: 105: SEQUENCE CHARACTERISTICS: LENGTH: 1481 base pairs
TYPE: nuclet acid STRANDEDNESS: single STRANDEDNESS: single STRANDEDNESS: single STRANDEDNESS: single STRANDEDNESS: cDNA
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RESULT 3
US-10-637-565-18
US-10-637-565-18
Sequence 18, Application US/10637565
Publication No. US20040043381A1
GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: PERRON, HAPEVE,
APPLICANT: FORMURAN-PRADE,
TITLE OF INVENTION: THE LITR REGION OF MSRV-1 AND THE PROTEINS IT ENCODES, AND PROBES PITTLE OF INVENTION: METHODS FOR DETECTING MSRV-1 RETROVIRUS
FILE REFERENCE: 110257
FILE REFERENCE: 110257
CURRENT APPLICATION NUMBER: US/10/637,565
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 08/979,847

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 39046A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1481; Conservative 0; Mismatches
                                                                                            APPLICATION NUMBER: US/10/114,104
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO: 105
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MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID
US-10-114-104-105
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1481 base pairs
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MATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
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OTHER INFORMATION: Incyte ID No. US20040043452A1 7477736CB1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOSTIC PROTECTION US/10416642

Sequence 4, Application US/10416642

Publication No. US2004004452A1

GENERAL INFORMATION:

APPLICANT: NCYTE GENOMICS, INC.

APPLICANT: ARVIZU, Chandra

ITLE OF INVENTION: EMBRYCGENESIS ASSOCIATED PROTEINS

FILE REFRENCE: PF-0842 PCT

CURRENT APPLICATION NUMBER: US/10/416,642

CURRENT FILING DATE: 2003-05-13

PRIOR APPLICATION NUMBER: 60/249,407

PRIOR FILING DATE: 2000-11-15

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 4

IENGTH: 2074
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ORGANISM: Homo s
FEATURE:
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                                                                                                                                                                      Query Match 100.0%; Score 1481; Best Local Similarity 100.0%; Pred. No. 0; Matches 1481; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US/09/890,340
PRIOR FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: PCT/IB00/00159
PRIOR APPLICATION NUMBER: EP 99420041.8
PRIOR FILING DATE: 1999-02-15
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 18
LENGTH: 2030
                                                                                                                ORGANISM: MSRV-1 retrovirus
                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (1)..(1626)
US-10-637-565-18
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Sequence 1, Application US/09902535
; Sequence 1, Application US/09902535
; Patent No. US20020102530A1
; GENERAL INPORMATION:
; APPLICANT: Keith, Jr., James C.
; APPLICANT: McCoy, John M.
; APPLICANT: McCoy, John M.
; TITLE OF INVENTION: Methods and compositions for diagnosing
; TITLE OF INVENTION: and treating preeclampsia and gestational trophoblast
; TITLE OF INVENTION: disorders
; TITLE OF INVENTION: disorders
; TITLE OF INVENTION: MUMBER: US/09/902,535
; CURRENT APPLICATION NUMBER: US/09/902,535
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/216,657
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FREEEE FARESE for Windows Version 4.0
; TENCING AND 1.
CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA 1200
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                                                        GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
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LOCATION: (930)...(2546)
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ORGANISM: Homo sapiens
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93.8%; Score 1389.8;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1424; Conservative 0; Mismatches
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           LOCATION: 1995
OTHER INFORMATION: a, t,
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                             ; OTHER INFORU
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Db 2070 CAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGGAACCTGTTTATTTTA 2129 1201 GGAGAAGAAGCGTTTATTGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA 1260 1201 GGAGAAGAATGCTGTTATTATGTTAATCCAGAATTGTCACTGAGAAAGTTAAAGAA 1260 1201 GGGGAAGAATGCTGTTATTATGTTAATCCAGAATCGTCACTGAGAAGTTAAAGAA 1289 1201 ATTCGAGATCGAATACAATGGAGGAGGAGGAACCTGAGAAGCTGGGGCCTC 1320 131 ATTCGAGATCGAATACAATGGAGGAGGAGGAGCTTCGAAACCTGGGGCCTC 1320 212 CTCAGCCAATGGAATGCTGAAGAGAGAGAGACTTCGAAACACTGGAGCCTCTAGGGCCTC 2249 225 CTCAGCCAATGGAATCCCCGGTTCTCCCCCTTCTAGGACCTCTAGCAGCTCTAATATTG 1380 225 CTCAGCCAATGGAATCCTCTTAACTTTAAGGACCTCTAGCAGCTTAATATTG 1380 Qy 1381 TTACTCCTCTTTGGACCCTGTAATCTTAAGGACCTCTAGGAGCTTCCAGAATT 1400 Qy 1411 GAAGCTGTAAAGCTACAGATGGTCTTTAACCTTCTTTAGGACCTCTTCCAGAATT 140 Db 2310 CTACTCCTTTTGGACCCTGTATCTTTAACTTTGTCTTTCCAGAATT 2369 Qy 1441 GAAGCTGTAAAGCTACAGATGGTCTTTAAAATTGTCTTCCAGAATT 2369 Qy 1441 GAAGCTGTAAAGCTACAGATGGTCTTTAAAATGTCAGAATC 2369 Db 2370 GAAGCTGTAAAACTACAAATGGAACCCCA 1481	RESULT 6 US-10-114-893-134 US-10-114-893-134 Sequence 134 Application US/10114893 Publication No. US202020193567A1 GENERAL INFORMATION: APPLICANT: Jacobs, Kenneth APPLICANT: LaVallie, Edward R. APPLICANT: Collins-Racie, Lisa A. APPLICANT: Treacy, Maurice APPLICANT: Preacy, Maurice APPLICANT: Spaulding, Vikki APPLICANT: Bowman, Michael R. APPLICANT: Bowman, Michael R. APPLICANT: Bowman, Michael R. APPLICANT: Spaulding, Vikki APPLICANT: Spaulding, Vikki APPLICANT: Spaulding, Viki APPLICANT: Spaulding, Viki APPLICANT: Bowman, Michael R. APPLICANT: Bowman, Michael R. APPLICANT: Bowman, Michael R. APPLICANT: Bowman, Michael R. APPLICANT: Bowman, Michael R. APPLICANT: Bowman, Michael R. APPLICANT: Spaulding, Viki APPLICANT: Bowman, Michael R. APPLICANT: Setting Daves: 2010,0114,893 CURRENT FILING DATE: 1999-10-06 NUMBER OF EXQ ID NOS: 321 SCOFTWARE: PatentIN Ver. 2.0 SEQ ID NO 134 LEMOTH: 2946 TTPE: DNA TTPE:	US-10-114-893-134 90.2%; Score 1335.4; DB 13; Length 2946; Best Local Similarity 93.9%; Pred. No. 0; Matches 1390; Conservative 0; Mismatches 91; Indels 0; Gaps 0; Matches 1390; Conservative 0; Mismatches 91; Indels 0; Gaps 0; Matches 1390; Conservative 0; Mismatches 91; Indels 0; Gaps 0; Matches 1390; Conservative 0; Mismatches 91; Indels 0; Gaps 0; Matches 1390; Conservative 0; Mismatches 91; Indels 0; Gaps 0; Matches 1390; Conservative 0; Mismatches 1390; Conservative 0; Mismatches 1390; Conservative 0; Mismatches 1300;
	21 AGCACCCCTAGGAGGACTAGTTCTCTCAAAAACTACATG 50 GGCACCTCTAGCCCCTACAAAGGACTAGTTCTCTCTCAAAACTACATG 10 GGCACCTCTAGCCCCTACAAAGGACTAGTTCTCTCTCAAAACTACATG 11	ACTGAACAAGATTTATACAATCTCTCTCTCTCTTTTAGTGCCCCCTATGACCATTTACAATCTTAGTGCTTCTTCTTAGTGCCCCCTATGACCATCTACAACAACAACAACAACAACAACAACAACATCTTACTTAGTGCTTCTTCTTAGTGCCCCCTTTAGTGCCATTAGTGCTTACTCTTAAGCCCCCCCTTTTGTTATACAATTATGTCATACTCTAAGCCCCCCCAACAAAAGAGTACCCATTTAGTATAACAATTATGTCATAGTCATAGTCATAGTGCTAGCATTGCCATTTGCTTATTGTTATAGAGCAGGAGTGCTAGGCAGAACAGGAACAGGAACAACATTTGTTATAGAGCAGGAGTGCTAGGCAGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACATTGTTTTTAACACTCCTTAGTTATATTTAACTCCCTAGCAGCAGTAACTTAGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACAGGAACATTAATATTAACACTCCTTAGAACAGCAGTCACTTAGAACAGAACTTAAATTGAGAACAGAACAGTCATTAATATTAACTCCCTAGCAGCAGTAACTTAAATTGAACAGAACAGTAAATTGAACAGAACATTAATATTAACTTCCTTAGAACTTAAATTGAACAGAACAGTAAATTGAAACAGAACATTAATATTAACTTCCTTAGAACAGCAGCAGTAACTTAATTTTAACTTCCTTAGAACTTAAATTTAAACTTCCTTAGAACAGCAGCAGTAACTTTATTTA

0 0 1321 CTCAGCCAATGGATGCCCTGGGTTCTTCCCCTTTAGGACCTCTAGTATTG 1380	RESULT 7 US-10-016-249-3 i Sequence 3, Application US/10016249 i Publication No. US20030100053A1 i GENERAL INFORMATION: i APPLICANT: Jacobs, Kenneth i APPLICANT: LaVallie, Edward R. i APPLICANT: Collins-Racie, Lisa A. i APPLICANT: Evans, Cheryl i APPLICANT: Evans, Cheryl i APPLICANT: Evans, Cheryl i APPLICANT: Werberg, David APPLICANT: Werberg, Maurice APPLICANT: Marberg, Maurice i APPLICANT: Mi Sha APPLICANT: Goode AJ172A i TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM FILE REFERENCE: GOOGE AJ172A i CURRENT PALICATION NUMBER: US/10/016,249 i CURRENT PALICATION NUMBER: US/10/10-20 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928 i RIOR APPLICATION NUMBER: US/09/175,928	Query Match 90.2%; Score 1335.4; DB 15; Length 2946; Best Local Similarity 93.9%; Pred. No. 0; 91; Indels 0; Gaps 0; Matches 1390; Conservative 0; Mismatches 91; Indels 0; Gaps 0; Qy 1 Argacccrcccrrarcarcrcrrarccrrraccrcrcarc 10 928 GCACCCCCTAATCATTTTTTCCTTTTACCCTTTTTACCTTCTACACCCTTCTCACC 987 Qy 121 ACGCGCTCCATGCTGTACAACAGTAGCTCCCTTACCAGAGTTTTCTATGAGA 1047 Qy 121 ACGCGCTCCATGCCGTATGACACCATCATATACCAGAGATTTTCTATGAGA 1047 Qy 121 ACGCGCTCCATCATGAGACACTCATATACACAGAGACTCTTTTTACAGGAAACCCC 1107 Qy 1048 ATGCAGCCCACACCCATATGCCCCATCATATACACAAGAGACCCC 1107 Qy 241 CATCACTGCCCACACCCATATGCCCCATCATATACTTCTACCACCACTTTGCATG 116 Qy 241 CATCACTGCCCACACCCATATGCCCCACACGCAACTGCTTCTCCTGCACCACTTTTGCATG 10 Db 1168 CATCACTACTTTTTTTTGACAGGAAAATGATTATCTCTGCACGATTTTTCCTGCAGAGACTT 120 Qy 241 CATCCAATTACTTTTTTTTTCTACCCAACTCTTTTTTTT
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                        Sequence 3, Application US/10133036
; Beduence 3, Application US/10133036
; Publication No. US20040054133A1
; GENERAL INFORMATION:
; APPLICANT: Conrad, Bernard
; APPLICANT: Mach, Bernard
; TITLE OF INVENITON: Multiple Sclerosis-Related Superantigen
; FILE REFERENCE: 23155-507
; CURRENT APPLICATION NUMBER: US/10/133,036
; CURRENT PILING DATE: 2002-04-26
; PRIOR PILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 3
; LENGTH: 1617
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 93.8%;
Matches 1389; Conservative
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                                          Score 1333.8;
Pred. No. 0;
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                                           Query Match 90.1%;
Best Local Similarity 93.8%;
Matches 1389; Conservative
 ; OTHER INFORMATION: hervl7
US-09-854-867-21
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US-09-854-867-21
US-09-854-867-21
SQUENCE 21, Application US/09854867
PUBLICATION NO. US20030224356A1
GENERAL INFORMATION:
APPLICANT: JOAN, KNOLL H
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
TITLE OF INVENTION SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
CURRENT APPLICATION NUMBER: US/09/854,867
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 613
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
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APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
APPLICANT: Bodress, Gregory
APPLICANT: Brown Meena
APPLICANT: Advances, Gregory
APPLICANT: Carter, Kennhard
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TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION Signature Gene Sets
CURRENT APPLICATION NUMBER: U.S. 60/236,891
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
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US-09-873-367C-81
Sequence 81, Application US/09873367C
Publication No. US20030165839A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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89.4%; Score 1324.2;
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APPLICANT: MALLET, Francois
APPLICANT: MALLET, Francois
APPLICANT: MALLET, Francois
APPLICANT: MALLET, Francois
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
TITLE OF INVENTION: AUTOIMMUNE 1100/632,793
CURRENT APPLICATION NUMBER: US/10/632,793
CURRENT FILING DATE: 2003-08-04
FRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: PCT/FR00/00144
FRIOR APPLICATION NUMBER: PCT/FR00/00144
FRIOR APPLICATION NUMBER: P99/0088
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
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LOCATION: (198)..(198)
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LOCATION: (1331)..(1331)
OTHER INFORMATION: n = a or
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NAME/KEY: misc_feature
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OTHER INFORMATION: n = a
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1662 1722 1602 CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC 1020 CTTCCTTTTGTTATAGGAGCAGGAGTGCTAGGTGCTAGGTACTGGCATTGGCGGTATC 1782 1062 1122 1182 1242 1302 1362 1422 1482 1542 1002 006 960 ö 780 840 420 480 540 009 099 720 942 240 300 360 822 120 882 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC 180 GGACCTCTTGTTTCCAATGTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT AATGGCTCTTCAGAATCTATGTGCTTCCTCATTCTTAGTGCCCCCTATGACCATCTAC ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACAAAAAAAGAGTACCCATT Arescerecerraterialitricierasisteritricaecerrateaecerece ACCTTCACTGCCCACCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG 943 ACCTICACTGCCCACACCCATATGCCCCGGAACTGCTATCACTCTGCCACTCTTTGCATG CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTTCAATC CAAAACCCTACTAACTGTGGATATGCCTCCCCTGAACTTCAGGCCATATGTTTCAATC CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCCACTTCCGTTTTAGTA GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAATTTT ATAGTCTGCCTACCCTCAGGAATATTTTTTTTGTCGTGCTACCTCAGCCTATCATTTTG CATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTAGTTGTCTGGAGGACTT CAAGGICAGGCAAGAAAAAAAAGAAGIAAAGGAAGCAATCTCCCAACTGACCGGGGACAT 421 AGCACCCCTAGCACAAAGGACTAGTTCTCTCAAAACTACATGAAACCTCCGTACC CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACAGA 823 GCACCCCCCCCATGCCGCTGTATGACCAGTAGCTCCCCTCACCCAGAGTTTCTATGGAGA GGAGCCACTGTCGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGTGGAATT Gaps

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1183 GGCACCTCTAGCCCCTACAAAGGACTAGATCTCTCAAAAACTACATGAAACCCTCCGTACC 1242
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                                                        ACCTICACTGCCCACACCCATATGCCCCCGCAACTGCTATCACTCTGCCACCTTTGCATG
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                                                                                                                       CATGCAAATACTCCATTATTGGACAGGAAAAATGATTAATCCTAGTTGTCCTGGAGGACTT
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 883 ATGCAGCGTCCCGGAAATATTGATGCCCCATCGTATAGGAGTCTTTCTAAGGGAACCCCC
                                                                                                     CATGCAAATACTCATTATTGGACAGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT
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| Sequence 26, Application US/200400482981|
| GENERAL INFORMATION:
| APPLICANT: PARANHOS-BACCALA, Glaucia APPLICANT: PARANHOS-BACCALA, Glaucia APPLICANT: PARANHOS-BACCALA, Glaucia APPLICANT: PARANHOS-BACCALA, Glaucia APPLICANT: PALLET, Francois APPLICANT: POISSET. Cecile
| TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN TITLE OF INVENTION: AUTOIMMUNE US/10/632,793
| FILE REFREENCE: 110048
| CURRENT APPLICATION NUMBER: US/10/869,927
| PRIOR APPLICATION NUMBER: US/09/869,927
| PRIOR APPLICATION NUMBER: PCT/FR00/00144
| PRIOR FILING DATE: 2000-01-21
| PRIOR FILING DATE: 1999-01-21
| NUMBER OF SEQ ID NOS: 33
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 26
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ORGANISM: Homo sapiens
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US-10-087-192-730/C

Sequence 730, Application US/10087192

Publication No. US20020182586A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Morris, David W.
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
CURRENT FILING DATE: 2.945.2001.2

CURRENT FILING DATE: 2.002-03-01

PRIOR FILING DATE: 2.000-12-22

PRIOR FILING DATE: 2.000-12-22

PRIOR FILING DATE: 2.000-12-03

NUMBER OF SEQ ID NOS: 2.059

SEQ ID NO 730

LUNGTH: PARLESQ for Windows Version 4.0

LUNGTH: 161334
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Pred. No. 0;
0; Mismatches
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LOCATION: (1)...(161334);

OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 92.5%;
Matches 1399; Conservative (
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ORGANISM: Homo sapiens
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H BONE MARROW, SIGNAL = 1.0
H LUNG, SIGNAL = 3.9
H HELA, SIGNAL = 7.2
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Pred. No. 0;
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Best Local Similarity 92.4%;
Matches 1218; Conservative
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US-09-864-761-4444
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Sequence 4444, Application US/99664761

Sequence 4444, Application US/99664761

Sequence 4444, Application US/99664761

SERVERAL INFORMATION:

PREPLICANT: Penn, SHARTON:

APPLICANT: Hanzel, David R.

ITIER OF INVERTION: BERESSION ANALYSIS BY MICROARRAY

TITIER OF INVERTION: GENE PERESSION ANALYSIS BY MICROARRAY

CURRENT FAPLICATION NUMBER: US/99/664, 761

CURRENT FAPLICATION NUMBER: US/99/664, 761

SHIGH SHART APPLICATION NUMBER: US/99/664

PRIOR FILING DATE: 2000-03-04

SHIGH SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHART SHAR
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REXPRESSED IN PLACENTA, SIGNAL = 20

REXPRESSED IN HBL100, SIGNAL = 6

REXPRESSED IN HEART, SIGNAL = 5.4

REXPRESSED IN BT474, SIGNAL = 5.9

REXPRESSED IN FETAL LIVER, SIGNAL = 1.9

REXPRESSED IN ADULT LIVER, SIGNAL = 1.9
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SOFTWARE: Annomax Sequence 1
SEQ ID NO 4444
LENGTH: 1894
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ORGANISM: Homo sapiens
FEATURE:
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US-10-632-793-24
US-10-632-793-24
| Sequence 24, Application US/10632793 |
| Publication No. US20040048298A1 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: PARAMHOS-BACCALA, Glaucia |
| APPLICANT: WOISSET, Cecile |
| TITLE OF INVENTION: ENDOGENCOUS NUCLEIC ACID FRAGWENT ASSOCIATED WITH AN TITLE OF INVENTION: AUTOIMMENDED DISEASE, LABELING METHOD AND REAGENT |
| TITLE OF INVENTION: ENDOGENCOUS NUCLEIC ACID FRAGWENT ASSOCIATED WITH AN TITLE OF INVENTION: 2003-08-04 |
| FILE REFERENCE: 110048 |
| CURRENT FILING DATE: 2003-08-04 |
| PRIOR PELICATION NUMBER: US/09/869,927 |
| PRIOR APPLICATION NUMBER: PR 99/00888 |
| PRIOR FILING DATE: 2000-01-21 |
| PRIOR FILING DATE: 2000-01-21 |
| PRIOR FILING DATE: 2000-01-21 |
| PRIOR FILING DATE: 1999-01-21 |
| SEQ ID NO 24 |
| LENGTH: 1948 |
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llarity 94.2%; Pred. No. 0;
Conservative 0; Mismatches
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (84)...(84)
OTHER INFORMATION: n = a or g
FEATURE:
NAME/KEY: misc feature
COTHER INFORMATION: n = a or g
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COTHER INFORMATION: n = a or g
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COTHER INFORMATION: n = a or g
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EXPRESSED IN BONE MARROW, SIGNAL = 6.3
EXPRESSED IN LUNG, SIGNAL = 3.9
EXPRESSED IN HELA, SIGNAL = 7.2
NT HIT: AF208161.1, EVALUE 0.0000+00
EST HUMAN HIT: AU138405.1, EVALUE 0.000+00
SWISSPROT HIT: P10269, EVALUE 2.000-16
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                                                                                                                                                                          Query Match 48.4%; Score 716.6; DB 9; Best Local Similarity 94.7%; Pred. No. 1e-209; Matches 753; Conservative 0; Mismatches 39;
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Publication No. US20040044181A1
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APPLICANT: BRILL BROWANTAL SHARTON G.
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TITLE OF INVESTION HUNDRE: US/09/664,761
CURRENT PLILING DATE: 2000-01-62-21
REIGN PELLORING NUNDRE: US/09/664,761
CURRENT PLILING DATE: 2000-01-64
PRICE PRICE REPUBLICATION NUNDRE: US/09/664,761
CURRENT PLILING DATE: 2000-01-64
PRICE PRICE REPUBLICATION NUNDRE: US/09/664
PRICE PRICE PRICE DATE: 2000-01-64
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N: EXPRESSED IN PLACENTA, SIGNAL = 20
N: EXPRESSED IN PLACENTA, SIGNAL = 6
N: EXPRESSED IN HEART, SIGNAL = 5.4
N: EXPRESSED IN HEART, SIGNAL = 5.9
N: EXPRESSED IN BT474, SIGNAL = 5.9
N: EXPRESSED IN PETAL LIVER, SIGNAL = 6.1
N: EXPRESSED IN ADULT LIVER, SIGNAL = 6.1
N: EXPRESSED IN BRAIN, SIGNAL = 6.2
                                                                                     GGAGAAGAACGCTGTTATTATGTTAATCAA 1230
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Patent No. US20020048763A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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 APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: 08/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
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                                                                                                                                                                                                                                                                Score 591.8; DB 16;
Pred. No. 4.8e-171;
0; Mismatches 7;
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US-10-632-793-19
Sequence 19, Application US/10632793
Sublication No. US20040048298A1
GENERAL INFORMATION:
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Matches 596; Conservative
                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (89)..(1684)
US-10-363-616-228
                                                                                                                                                                         ORGANISM: Homo sapiens
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GENERAL INFORMATION
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APPLICANT: PARANHOS-BACCALA, Glaucia

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APPLICANT: VOISSET, Cecile
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/10/632,793
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2001-10-22
PRIOR PILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/FR00/00144
PRIOR APPLICATION NUMBER: PS 99/00888
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
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99.7%; Pred. No. 1.6e-168;
iive 0; Mismatches 2;
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Matches 584; Conservative
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NAME/KEY: misc feature
LOCATION: (305)..(305)
OTHER INFORMATION: n = a or g or c or t/u
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ORGANISM: Homo sapiens
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## APPLICANT: VOISSET, Cecile
### TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
### TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
### TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
### FILE REFERENCE: 110048

**CURRENT APPLICATION NUMBER: US/99/869,927

### PRIOR APPLICATION NUMBER: US/99/869,927

### PRIOR FILING DATE: 2001-10-22

### PRIOR FILING DATE: 2000-01-21

### PRIOR FILING DATE: 1999-01-21

### PRIOR FILING DATE: 1999-01-21

### RIOR FILING DATE: 1999-01-21

### NUMBER OF SEQ ID NOS: 33

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91.8%; Pred. No. 5.9e-148;
tive 0; Mismatches 49;
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Publication No. US20040048298A1;
GENERAL INPORMATION:
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: MALLET, Francois;
APPLICANT: VOISSET, Cecile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
US-10-632-793-25
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US-10-632-793-23
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TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN FILLE REFERENCE: 110048

CURRENT APPLICATION NUMBER: US/10/632,793

CURRENT APPLICATION NUMBER: US/09/869,927

PRIOR APPLICATION NUMBER: US/09/869,927

PRIOR APPLICATION NUMBER: PCT/FR00/00144

PRIOR FILING DATE: 2000-10-22

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 1999-01-21

PRIOR FILING DATE: 1999-01-21

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN VERSION 3.1

SOFTWARE: PATENTIN VERSION 3.1

LENGTH: 2006
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Best Local Similarity 93.2%; Pred. No. 6.9e-147,
Matches 548; Conservative 0; Mismatches 39,
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; Sequence 322491, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
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403 TCACTCACTCCATGCTGYTGTATGACCAGTAGCTCCCCTTACCACGAGTTTCT-TGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                 25.5%; Score 377.8; DB 13; Length 90.7%; Pred. No. 2.6e-105; Live 2; Mismatches 39; Indels
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LOCATION: (1)...(570)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 90.7
Matches 411; Conservative
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APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PLILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PLILOR DATE: 2000-04-20
PRIOR PLILOR DATE: 2000-03-29
PRIOR PLILOR DATE: 2000-03-29
PRIOR PLILOR DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 ATGCAGCTTCCTGGAAATATTGATTCCCCATCATATAGGAGTTTATCTAAGGGAAATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ACCTICACTGCCCACACCCATAIGCCCCGCAACTGCIAIAACTCTGCCACTCTTTGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 CATGCAAATACTCATTATTGGACAGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GGAGCCACTGTCTGTTGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGGTGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCACCCTAGACCTACAAAGGACTAATCCCC 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)...(570)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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US-10-027-632-322491/c
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; Sequence 322492, Application US/10027632 ; Publication No. US20020198371A1

RESULT 23 US-10-027-632-322492/c

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Sequence 322492, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGCCACTGTCTGTTGGACTTACTTCACCCCTACCAGTATGTCTGATGGGGGTGGAGTT 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGATCAGGCAAGAAAAAAAACACGTAAAGGAAGTAATCTCCCAACTGACCCTGGTACAT 45
                           GENERAL, INCREMENTION:

APPLICANT: Wang, David G.

TITLE OF INVERTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR PILING DATE: 2000-07-12

PRIOR PLING DATE: 2000-07-29

PRIOR PLING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-08-09

PRIOR PLING DATE: 1999-08-09

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.5%; Score 377.8; DB 1: 90.7%; Pred. No. 2.6e-105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: (1)...(570)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-322491
    US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 90.7
Matches 411; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
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GCACCCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC 180
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GENERAL INFORMATION:

APPLICANT' Mang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR PELICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-07-12

PRIOR PELICATION NUMBER: US 60/198,676

PRIOR PELICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-10-02-8

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SEQ ID NO 322492

LENGTH:: 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 AGCACCCTAGCCCCTACAAAGGACTAGTTCTC 453
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RESULT

RESULT 25 US-10-027-632-322492/c

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341 CATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTAGTTGTCCTTGAGGACTT 400
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.8%; Score 353; DB 13; Best Local Similarity 92.0%; Pred. No. 1.1e-97; Matches 412; Conservative 2; Mismatches 30;
               PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PSESEQ for Windows Version 4.0
SOFTWARE: PSESEQ for Windows Version 4.0
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OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Human
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                                                                                                        APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Barzel, David R.
APPLICANT: Barzel, David R.
APPLICANT: Barzel, David R.
APPLICANT: Lavid RENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOUTCA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFWARE: Annomax Sequence Listing Engine vers. 1.1
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Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.81

OTHER INFORMATION: EST HUMAN HIT: BE73434.1, EVALUE 0.00000

OTHER INFORMATION: WISSPROT HIT: P10269, EVALUE 4.000-26

OTHER INFORMATION: NT HIT: AF208161.1, EVALUE 0.0000+00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Indels
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24.6%; Score 364; DB 15;
Best Local Similarity 91.7%; Pred. No. 4.4e-101;
Matches 385; Conservative 0; Mismatches 35;
                      Sequence 4312, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
US-10-029-386-4312/c
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PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/199,676
PRIOR PTLING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PRASEEQ for Windows Version 4.0
LENGTH: 551
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                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human
FEATURE:
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Publication No. US20030204075A9
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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23.8%; Score 353; DB 13;
Best Local Similarity 92.0%; Pred. No. 1.1e-97;
Matches 412; Conservative 2; Mismatches 30;
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-09-8
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-8
PRIOR PILING DATE: 1999-09-8
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTESEQ FOR WINDOWN VERSION 4.0
SERIOTH: 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                 | NAME/KEY: misc_feature
| LOCATION: (1)...(551)
| OTHER INFORMATION: n = A,T,C or G
US-10-027-632-322575
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102 ATGGCCCTCCCTTATCATATTTTTCTCTTTACTGTTCTCTTACCCTCTTTCACTCTCACT
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Publication No. US20030204075A9
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERRENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
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                                                                                                                                                                          Query Match 23.8%; Score 353; DB 15; Length 551; Best Local Similarity 92.0%; Pred. No. 1.1e-97; Matches 412; Conservative 2; Mismatches 30; Indels
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LOCATION: (1)...(551)
OTHER INFORMATION: n = A,T,C or G
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121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATAGGAGTTTATCTAAGGGAAACTCC 180
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23.8%; Score 353; DB 15; Length 551;
Best Local Similarity 92.0%; Pred. No. 1.1e-97;
Matches 412; Conservative 2; Mismatches 30; Indels
             CORRELIANCE DATE: 2002

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/166,358

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-38

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PRIOR PILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

LENGTH: 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
| DCCATION: (1)...(551)
| DCTHER INFORMATION: n = A,T,C or G
US-10-027-632-322575
2002-04-30
CURRENT FILING DATE:
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score:

Perfect

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Direct Submission
Submitted (20-JUJ-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CR622175 21-JUL-2004 tull-length cDNA clone CSODI051YM13 of Placenta Cot 25-normalized
                                                   ba84f03.y
602593490
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BX450495 BX450495
BX365066 BX365066
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BX380176
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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0; Mismatches
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/dolone="csOD1051YM13"
/tissue_type="Placenta Cc
/plasmid="pcMvSpORT_6"
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BX430055
BE019603
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BX365066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Homo sapiens (human).
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HTC; CNSLT_CDNA.
Homo sapiens (human)
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Matches 1389; Conservative
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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seq length: 200000000
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Qy 1141 CAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGAACCTGTTTATTTTA 1200 Db 1670 CAAAATCGAAGAGCTTTAGCTAACCGCTGAAAGAGGGGAACCTGTTTATTTTA 1729 Qy 1201 GGAGAAGAAGCTTTATTATTTATTTATTTTATTTTTATTTTATTTTATTTT	2716 bp mRNA linear 5 CSODE013Y120 of Placenta of 76 76 76 76 8 Catarrhin; Hominidae 8 Esse, J. and Polayes, D. 8 aries and normalization 8 and normalization 8 and normalization 8 and normalization 8 and normalization 8 and normalization 8 and normalization 8 and normalization 8 and normalization 8 Esse, J. and Polayes, D. 8 and normalization 8	Query Match 90.1%; Score 1333.8; DB 3; Length 2716; Best Local Similarity 93.8%; Pred. No. 0; Matches 1389; Conservative 0; Mismatches 92; Indels 0; Gaps 0; Qy 1 AUGGCCCTCCTTATCATTACTATACTGTTCTTTACCCCCTTTCGCTCTCACT 60 Db 773 ATGGCCCTCCTTATCATATTTTCTCTTTACCGTTCTTTACCCTCTTTCACTCTTCACT
61 GCACCCCTCCATGCTGCTGTACAACCAGTAGCTCCCTTACCAAGAGTTTCTATGAAGA 120		1021 ACAACCTCTACTCAGTTCTACTACAAACTATCTCAAGAATAAATGGTGACATGGAACAG 1080

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	CR605851 LOCUS LOCUS DEFINITION Full-length cDNA clone CSODE012YJ24 of Placenta of Homo sapiens (human). ACCESSION ROCOSSI NERSION REGOSSI.1 GI:5048658 HTC; CNSLT_CDNA. SOURCE HOMO sapiens CR605851.1 GI:5048658 HOMO sapiens CR605851.1 GI:5048658 HOMO sapiens CR605851.1 GI:50486658 AUTHORS Li,W.B. Gruber, C. Jessee, J. and Polayes, D. AUTHORS Li,W.B. Gruber, C. Jessee, J. and Polayes, D. TITLE JUDUDIished TITLE JUDUDIished REMARK CONTACT: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 REFERENCE Z (bases 1 to 2748)	AUTHORS Genoscope. TILLE Direct Submission JOURNAL Submission JOURNAL Submission JOURNAL Submission JOURNAL Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.	Query Match Best Local Similarity 93.8%; Pred. No. 0; Matches 1389; Conservative 0; Mismatches 92; Indels 0; Gaps 0; Qy 1 ATGGCCTCCCTTATCATATCTTTATCTCTTACCCCTTTGGCTCTCACC Db 772 ATGGCCTCCTTATCATATTTTCTTTTACTGTTCTTTACCCTTTTACTCTTTACCCTTTACTCTTTACTCTTTACCCTTTACTCTTATGAAGA 120
61 GCACCCCTCCATGCTGCTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120 833 GCACCCCTCCATGCCGCTATACAACCAGTAGCTCCCTTACCAAGAGTTTCTATGAGGA 892 121 ACGCGGCTTCCTGGAATATTGATGCCCCTAATACAGAGTTTCTAAGGGAAACTCC 180 893 ATGCAGCCCCCGCAAATATTGATGCCCCATCATAAGAGGTTTCTAAGGGAAACTCC 180 181 ACCTTCACTGCCCCAAATATTGATGCCCCAACTGCTATAAGAGCTTTTTTTT	AGCACCCCTAGGAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC	721 AGCAATACTATAGACACACCTCCCAATGCATCGGGGGGACACCTCCCCACACCA 780 1493 AGCAATACTACTACACACACCTCCCAATGCATCGGGGGGACACCTCCCCACACCA 151 1493 AGCAATACTACACACACCCAATGCTTTTTTTTTTTTTTT	1021 ACAACCTCTACTCAGTTCTACTACAAACTATCTCAAGAATAAATGGTGACATGGAACAG 1080

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                        CR625046 2748 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI044YK06 of Placenta Cot 25-normalized of Homo sapiens (human).
CAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTATTTTA 1971
                                                                             ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTC 1320
                                                                                                                             CTCAGCCAATGGATGCCCTGGGTTCTCCCTTTAGGACCTCTAGCAGCTCTAATATTG 1380
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D. Pull.-length, CDNA libraries and normalization
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                                                                                          2092 CTCAGCCAATGGCCCTGGATTCTCCCCTTCTTAGGACCTCTAGGACTATAATATTG
                           GGAGAAGGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA
                                        Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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llarity 93.8%; Pred. No. 0;
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CR625046.1 GI:50505853
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Homo sapiens (human)
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                                             ACGCGCCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC
                                                            ATGCAGCGTCCCCGGAAATATTGATGCCCCATCGTATAGGAGTCTTTCTAAGGGAACCCCC
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                                                                                                ACCTICACTGCCCACACCCATATGCCCCGCAACTGCTATAACTCTGCCACCTTTTGCATG
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BP 191 91006 EVRY cedax - France
Email: sequencefogenoscope.cns.fr, Web : www.genoscope.cns.fr
Int strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/clone lib="Homo sapiens Placenta"
/note="lib="Homo sapiens primed with a NotI-oligo (dT)
/primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (Dases 1 to 935)

1 (A.M.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)

Contact: Genoscope
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                     CTCAGCCAATGGATGCCCTGGGTTCTCCCTTTAGGACCTCTAGCAGCTCTAATATTG
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iive 0; Mismatches 53;
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/mol_type="mRNA"
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Ist strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster

Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)

Contact: Genoscope

For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAE023ZF07_AE02167_1&c=4215.r

Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:96"
/db_xref="taxon:901051YM13"
/clone="Colone:Ype="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR vices of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TGTCCTGGAGGACTTGGAGTCACTGTTGGACTTACTTCACCCAAACTGGTATGTCT
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Pred. No. 1.9e-229;
0; Mismatches 56;
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93.7%;
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EST 08-APR-2004

BX347952

WAS Homo Bapiens PLACENTA COT 25-NORWALIZED Homo Sapiens CDNA CLONE (SODIO51YM13 5-PRIME, mRNA BEQUENCE.

RESULT 7 BX347952 LOCUS DEFINITION

BX347952.1 GI:30375235 Homo sapiens (human)

KEYWORDS SOURCE ORGANISM ACCESSION VERSION

REFERENCE

Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Banmanlia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 955)

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BX326647 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI051YM13 3-PRIME, mRNA sequence.
BX326647
BX326647.1 GI:30334578
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121 AAAAGAAGTAATCTCCCAACTCACCCGGGTACATGGCACCTCTAGCCCCTACAAAGGACT
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BP 191 91006 ENRY Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized, Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                   CCTATGACCATCTACACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACAAC
                      GCCTATCATTGTTTGAATGGCTCTTCAGAATCTATGTGCTTCCTCCTTCTTAGTGCCC
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                                                                                                                                                                                                                                                                                                                                                      900 TAGCAGCAGNAGTTCCTTCAAAATCGAAGAGGCTTAGACTTGCTACCCGC
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Pred. No. 3.1e-211;
0; Mismatches 65;
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Homo sapiens
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997

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Contact: Genoscope Control of Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAA008ZH03_CS00697_2&c=4215.r
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Homo sapiens cDNA clone CS0DE013YI20
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                                                                                                                                                                                                                                                                                              TAGGTACTGGCATTGGCAGTATCACAACCTCTACTCAGTTCTACTACAAACTATCTCAAG 1057
                                                                                                                           937
                                                                                                                                                 273 TAGTIGCCCCCTATGACCATCTACACTGAACAAGATTTATACAGTTATGTCATATCTAAGC 214
                                                                                                                                                                                                                                                  213 cccgcaacaaaaaaacraccarrcrrccrrrrgrraragaacaacaacracracacac 154
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 903)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30648825.
                                                                                                                                                                                                                                                                                                                                                                                                    153 radgracrescarrescegararcacaaccreracrescretacracracaacrarereas 94
                                                                   GTACCTCAGCCTATCGTTGTTTGAATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCT
                                                                                                                           TAGTGCCCCCTATGACCATCTACACTGAACAAGATTTATACAATCATGTCGTACCTAAGC
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BX408752 Homo sapiens PLACENTA
5-PRIME, mRNA sequence.
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                                                                                                                                                                Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecok V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                              For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAD010zC11_AD00948_1&c=4215.r
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone=lib="Homo sapiens primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 872)
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                                                                                                     Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/clone="CS0DI051YM13"
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Contract: varioscope and the sequencage genoscope. Centre National de Sequencage BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France Email: sequencacope.cns.fr. Web: www.genoscope.cns.fr Bmail: sequence Gagenoscope.cns.fr, Web: www.genoscope.cns.fr into the Not I and cloned into the Not I and Ecory sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAA008ZEOZ_CSO0686_l&c=4215.r
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      Vertebrata; Euteleostomi;
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          Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
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        Bukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Butheria; Primates; Catarrhini; Hon
1 (bases 1 to 883)
Li,W.B.; Gruber,C.; Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 737.2; DB 5;
Pred, No. 8.7e-207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
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BX408733 GI:30635957 ESY.
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                                         GCCCTCCCTTATCATACTTTTCTCTTTACTGTTCTTTACCCCCTTTCGCTCTCACTGCA
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      93.0%;
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Homo sapiens
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                                             TAAAAACCAACCCTCATGGGCTCCATGAGTNCTCGGGCCAAAAAACCCTACTAACTGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 AGGAGTGCTAGGTGCACTAGGTACTGGCATTGGCGGTATCACAACCTCTACTCAGTTCTA
                     TTAATACCACCCTCACTCGCTCCATGAGGTCTC-AGCCCAAAACCCTACTAACTGTTGG
                                                                                                       ATGTGCCTCCCCTGCACTTCAGGCCATACATTTCAATCCCTGTTCCTGAACAATGGAAC
                                                                                                                             ATATECCTCCNCCTGAACTTCAGGGCATATGTTTCAATCCCTGTACCTGAACAATGGAAC
                                                                                                                                                                                       AACTTCAGCACAGA-AATAAACACCACTTCCGTTTTAGTAGGACCTCTTGTTTCCAATCT
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAD009ZB06_AD00811_1&c=4215.r
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to sapiens cDNA
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="manka"
//do xref="taxon:9606"
/db xref="taxon:9606"
/clone="CSOD1022Y1018"
/clone_Tib="PLACENTA COT 25-NORWALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/clone_Tis strand cDNA was primed with a NotI-oligo(dT)
/note="ist strand cDNA was primed with a NotI-oligo(dT)
/note="ist strand cDNA was primed with a NotI oligo(dT)
/note="ist strand cDNA was grimed with a NotI oligo(dT)
/note="ist strand cDNA was grimed inco the Not I and EcoR vaites of the pCMVSPORT 6 vector. Library was normalized.
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                                                              TCCCCCTGAACTTCAGGCCATATGTTTCAATCCCTGTACCTGAACAATGGAACAACTTCA
                                                                                                                                                GCACAGAAAATAAACACCACTTCCGTTTTAGTAGGACCTCTTGTTCCAATCGGAAATAA
                                                                                                                                                                                                                                                 AATGCATCAGGGTGGGTAACTCCTTCCACACAATAGTCTGCCTACCCTCA-GAATATTT
                                                                                                                        GCACAGAAATAAACACCACTTCCGTTTTAGTAGGACCTCTTGTTTCCAATCTGGAAATAA
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CCACCCTCACTGGGCTCCCATGAGGTCTCGGCCCAAAACCCTACTAACTGTTGGATATGCC
                                        TCCCCCTGCACTTCAGGCCATACATTTCAATCCCTGTTCCTGAACAATGGAACAACTTCA
                                                                                                                                                                                                        CCCATACCTCAAACCTCACCTGTGTAAATTTTAGCAATACTATAGACAACCAGCTCCC
                                                                                                                                                                                                                                                                                          AATGCATCA - GGTGGGTAACACCTCCCACACGAATAGTCTGCCTACCCTCAGGAATATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX347619
BX347619 Homo sapiens PLACENTA COT 25-NORMALIZED Homo clone CSODI022YJ18 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTCTCATTCTTAGTGCCCCCTTATGACATTCTACACTGAACAAG 882
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Pred. No. 3.5e-204;
0; Mismatches 55;
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BX347619.1 GI:30379218
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Best Local Similarity 93.2
Matches 803; Conservative
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BX347619/c
LOCUS
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1. 921
/ organism="HOmo sapiens"
/ organism="HOmo sapiens"
/ mol_type="mRNA"
/ db xref="taxon:9606"
/ clone="CSODE012YJ24"
/ tissue type="PLACENTA"
/ clone lib="Homo sapiens PLACENTA"
/ clone lib="tomo sapiens PLACENTA"
/ clone lib="tomo colored"
/ double-strand cDNA was digested with Not I and cloned into the Not I and EcoNY sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Bmail: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
Estand CDNA was primed with a NotI-oligo(dT) Primer. Five prime
1st strand cDNA was primed with a NotI-oligo(dT) Primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            division of Invitrogen.
This sequence belongs to sequence cluster, see
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAA008ZE02_CS00686_2&c=4215.r
                                                                                                                                                                                                                                                                                                                                                                         1343
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                                                                                                                                                                                                                                                                                                   TAATCAATCCGGAATCGTCACTGAGAAGTTAAAGAAATTCGAGATCGAATACAACGTAG 116
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                  GCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGACTT 236
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                       gernaaceergaaagagagaacergrrrarrrrragagaaaaaaaaceergrrarrarer
                                                                                                                                                                                                                                    1224 TAATCAATCCAGAATTGTCACTGAGAAGTTAAAGAAATTCGAGATCGAATACAATGTAG
                                                                                                                                                                                                                                                                                                                                                                            1284 AGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCTTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                          115 AGCAGAGGAGCTTCGAAACACTGGACCTGGGGCCTCCTCAGCCATGGATGCCCTGGAT
                                                                                        GCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTTAGGAGAAGAACGCTGTTATTATGT
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 1.2e-198;
0; Mismatches 98;
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BX408734
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                                                                                                                                                                                                                             Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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sites of the pCMVSPORT 6 vector. Library was normalized."
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Contact: Genoscope
Primates; Catarrhini; Hominidae; Homo
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                      1 (bases 1 to 836)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/clone="CSODI044YK06"
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                                                                         AUTHORS
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7108.r

Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)

For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAU010ZB08_U0922_1&c=7108.r. Location/Qualifiers

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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.

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   Length 844;
                                         Indels
 Score 705.8; DB 5;
Pred. No. 1.8e-197;
0; Mismatches 58;
47.78;
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   Query Match
Best Local Similarity
Matches 762; Conserv
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BX347111 BX347111 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens CDNA clone CSODI022YE21 3-PRIME, mRNA sequence. BX347111

BX347111.1 GI:30375145 Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

RESULT 15 BX347111/c LOCUS Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 844)

us-09-319-156b-9.rst

Db 128 CTCTTTGCATGCAAATACTCATTATTGGACAGGAAAATGATTAATCCTAGTTGTC 187	OY 530 AGGTCTCAGCCCAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCAT 589	QY 770 CTCCCACACGAATAGTCTGCCTACGCTAGGAATATTTTTGTCTGTGGTACCTCAGCCT 829 bb 668 CTCCCACACAAATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGTTACCTCAACT 727 QY 830 ATCATTGTTTGAATGGCTCTTCAGAATCTATTGTTCTTAGTGCCCCCTA 889 Db 728 ATCGTTGTTTGAATGGCTC-TCAGAATCTATGGGCTTCCTCTCTTTAGGGCCCCCCTA 786 QY 890 TGACCATCTACACTGAACAAGATT 913 Db 787 TGACCATCTACACTGAACAAGATT 810	RESULT 17 BX368078/C LOCUS BX368078	REFERENCE 1 (bases 1 to 846) AUTHORS Li,W. B., Gruber,C., Jessee,J. and Polayes,D. AUTHORAL Full-length cDNA libraries and normalization JOURNAL GOMENT CONTACT: Genoscope Control on May 8, 2013 this sequence version replaced gi:30447710. COMMENT CONTACT: Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 ENRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Ist strand cDNA was primed vith a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
Qy 1100 CCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTTCAAAATCGAAGACTTTAG 1159 Db 237 CCTTGCAAGATCAACTTAACTCCCTAGCAGGAGTACTACAAATCGAAGATTTAG 178 Qy 1160 ACTTGCTAACCGCCAAAGAGGGGGAACCTGTTTATTTTTAGGAGAAGATTTATT 1219 Db 177 ACTTGCTAACCGCCAAAGAGGGGGAACCTGTTTATTTTTAGGAGAAGATGCTTTATT 118 Qy 1220 ATGTTAATCAATCCAGGAAACTGACAAAGATTAATTTTTAGGAAAGAATTATT 118 Db 117 ATGTTAATCAATCCAGGAAATGTCACTGAGAAAGTTAAAGAAATTCGAGATCAATTATT 118 Db 117 ATGTTAATCAATCCAGGAAATGTCACTGAGAAAGTTAAAGAAATTCGAGATCAAACAAC 58 Qy 1280 GTAGAGGAGGGCTTCAAAACACGGAAACGTGAGGGCCTCC 1321 Qy 1280 GTAGAGGAGGCTTCAAAACACGGAACCGGGGGCCTCC 1321 Db 57 GTAGAGCAGAGGAGGCTTCAAAACACTGGAACCTGGGGCCTCC 16 Db 57 GTAGAGCAGAGGAGCTTCCAAAACACTGGAACCTGGGGCCCCC 16	BESULT 16 BESS 57907 BESS 57907 LOCUS LOCUS BESS 57907 BEFINITION BX367907 BOORD ELACENTA COT 25-NORMALIZED Homo sapiens CDNA CLOCUS BX367907 CLOCUS BX367907 CLOCUS BX367907 CLOCUS BX367907 BX		H CG	Ouery Match Best Local Similarity 93.8%; Score 703.2; DB 5; Length 828; Best Local Similarity 93.8%; Pred. No. 1e-196; Matches 754; Conservative 0; Mismatches 48; Indels 2; Gaps 2; Oy 110 TTCTAGGAGACGCGCTTCCTGGAATATTGATGCCCCATCATATGGAGTTTATCTA 169 Db 9 TTCTTGGAGAACTCCCACCCATATGCCCCCATCGTATAGGAGTTTTTTA 67 Oy 170 AGGGAAACTCCACCCCCCACCCATATGCCCCCGCAACTGTTTATCTA 67 Oy 170 AGGGAAACTCCACTCACTGCCCCACACATGCCCCGCAACTGCTTATATCCCC 229 Oy 170 AGGGAAACTCCACTCACTGCCCACACATGCCCCGCAACTGCTATACCCCA 127 Oy 170 AGGGAAACTCCACTCACTCACTCATTATTGGACACTGCTATCACTCTGCCA 127 Oy 230 CTCTTGCATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTGCCA 127 OY 121

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        For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAU012ZDO5_U01092_1&c=4215.r. Location/Qualifiers
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Pred. No. 2.4e-195;
0; Mismatches 56;
                                                         organism="Homo sapiens"
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92.8%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (basea 1 to 995)

2. 1 (basea 1 to 995)

3. 1i, W. B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

1. Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30462931.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EWRY cedex - France

BP 191 91006 EWRY cedex - France

BP 191 91006 EWRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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/db xref="taxon:9606"
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/clone="type="placenta"
/clone=lib="Homo sapiens Placenta COT 25-NORWALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was digested with not I and cloned into the Not I and BCOR V sites of the pCMVSPORT 6 vector. Library was normalized."
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BX389657 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI051YM13 5-PRIME, mRNA sequence.
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                        66 ACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAACGT-GAGCAGAGGAGCTTCGAAAC
1243 ACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAAC
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86.8%; Pred. No. 1.3e-194;
tive 0; Mismatches 114;
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1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
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| primer. Pive prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Pred. No. 2.9e-194;
0; Mismatches 57; Indels
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    division of Invitrogen. This sequence belongs
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AQ261133 631 bp DNA linear GSS 24-OCT-1998 CITBI-E1-2506C15.TF CITBI-E1 Homo sapiens genomic clone 2506C15, genomic survey sequence.
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Seg primer: Mi3-21
Class: BAC ends.
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                                                       363 GTCATATCTAAGCCCCCGCAACAAAGAGTACCCATTCTTCCTTTGTTATAGGAGCAGGA
                                       925 GTCGTACCTAAGCCCCACAACAAAAGAGTACCCATTCTTCCTTTTGTTATCAGAGCAGGA
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/clone lib="CITBI-E1"
/note="Vector: pBeloBAC11;
CalTech Human BAC Library D
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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GSS.
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831 AGCCATACTACATACACAAACCAAATTCCCATGCATCAAGGTGGTAACTCCTCCCACACA 889
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 723)

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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human CDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                           Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCCTCCCCCTGAACTTCAGGCCATATGTTTCAATCCCTGTACCTGAACAATGGAACAAC
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AU138405 PLACE1 Homo sapiens CDNA clone PLACE1008489 5', mRNA
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43.7%; Score 647; DB 1; Length 723;
Best Local Similarity 94.6%; Pred. No. 4.7e-180;
Matches 679; Conservative 0; Mismatches 38; Indels
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/clone lib="PLACE1"
/note="Vector: pME18SFL3"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1008489"
                                 AU138405.1 GI:10999926
                                                                                                                                                                                                                                                                                                                                                                                                                  human cDNA project
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Contact: Takao Isogai
Genomics Laboratory
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BX409328 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE013XI20 5-PRIME, mRNA sequence.
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science; University of Tokyo, and Helix Research Institute.

Location/Qualifiers
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1. 702
//crganiam="Homo sapiens"
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Pred. No. 1.3e-174;
0; Mismatches 37;
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                                                                                                /mol type="makk"
/db_xref="taxon:9606"
/clone="plAcE1007839"
/tissue_type="placenta"
/clone lib="placenta"
/note="Vector: pME18SFL3"
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Best Local Similarity 94.6%;
Matches 660; Conservative
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                                                                                                      CAAAGGACTAGTTCTCTCAAAACTACATGAAACCTCGGTACCCATACTCGCCTGGTGAG 497
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                                                                 CAAAGGACTAGTTCTCTCACAAAACTACATGAAACCCTCCGTACCCATACTCGCCTGGGGAG
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                                                 AAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACATAGCACCCCTAGCCCCTA
                       Gaps
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                       Indels
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
       Pred. No. 7.4e-175;
0; Mismatches 1;
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
          99.88;
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Homo sapiens (human)
                        630; Conservative
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us-09-319-156b-9.rst

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Dases 1 to 714)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE734284 114 bp mRNA linear EST 15-SEP-2000 601565487F1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:3840572 5',
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following s' adaptor: GGCACGAG(G). Size-selected >500pp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University)
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/clone="IMAGE:3840572"
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BP 191 91006 EVRY cedex - France
Email: sequenceSope.cns.fr, Web : www.genoscope.cns.fr
Email: sequenceGenoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCHVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invirrogen.
This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAE012ZF02_AB01071_1&c=4215.r
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/clone_lib="Homos sapiens PLACENTA"
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On May 13, 2003 this sequence version replaced gi:30652931
Contact: Genoscope
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/clone="CS0DE013Y120"
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                                                                       Homo sapiens (human)
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On May 15, 2003 this sequence version replaced gi:30776872.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAB002ZD11_CSO0181_1&c=4215.r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 580.4; DB 5;
Pred. No. 2.6e-160;
0; Mismatches 41;
                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.6%;
Matches 616; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              TCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATCAC 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACTGACTCCCTGGTCACCTTGCAAGATCAACTTCCCTAGCAGCAGTAGTCCTTCA 1142
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1. (bases 1 to 658)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                          AGTCTGCCTACCCTCAGGAATATTTTTTTGTCTGTGGTACCTCAGCCTATC-GTGTTTGAA 119
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           ZAP-cDNA synthesis kit
RT (Life Technologies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCTCTTCAGAATCTATGCTTCCTCATTCTTAGTGCCCCCTATGACCATCTACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1203 AGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAAAT
                                                                                                                                                                                                      AGTCTGCCTACCCTCAGGAATATTTTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTGAA
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                                                                                                                                       CAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACACGAAT
                                                                                                                                                                       CAATACTACATACACAACCAACTCCCAATGCATCAGGTGGGTAACTCCTCCCACACAAAT
                                                                                                         Gaps
                                                                                                         4.
                                                                          714;
                                                                          Length
                                                                                                         Indels
                                                                          Score 609.8; DB 2;
Pred. No. 5e-169;
0; Mismatches 37;
           of California, Berkeley) using (Stratagene) and Superscript II
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BX430050.2 GI:47003301
                                                                          41.2%;
94.3%;
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Homo sapiens
                                                                                                         676; Conservative
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TITLE
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VERSION
KEYWORDS
SOURCE
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BX430055 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE013YI20 3-PRIME, mENA sequence.

BX430055.2 GI:47006728
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/tissue type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: PCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAB002ZG11_CS00184_1&c=4215.r
                                                                                                                                             361 AAGAAGNAATNTNCCAACTAACCCGGNTACATGGCACCTNTAGCCCCTACAAAGGACTAG 420
                                                                                                                                                                                                                                421 ATCTCTCAAAACTACATGAAACCCTCCGNACCCATACTCGCCTGGNAAGTCTATTNAATA 480
                                                                    301 CCCAAACTGGTATGTCTGATGGGGGTGGAGTTCAAGATCAGGCAAGAAAAAACATGNAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    629 GCACAGAAATAAACA-CCACTTCCGTTTTAGTAGGACCTCTTGTTTCCAATCTGGAAATA 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 TTCTCTCAAAACTACATGAAACCCTCCGTACCCATACTCGCCTGGTGAGCCTATTTAATA
                                                                                                                                                                                                                                                                                                                    481 CCACCCTCACTGNCCTCCATGAGGTTTCGTTCCAAAACCCTACTAACTGCTGTATATGCC
                                                                                                                                                                                                                                                                                                                                                                                569 TCCCCCTGCACTTCAGGCCATACATTTCAATCCCTGTTCCTGAACAATGGAACAACTTCA
                             CCCATACCAGTATGTCTGATGGGGGTGGAATTCAAGGTCAGGCAAGAGAAAAACAAGTAA
                                                                                                                389 AGGAAGCAATCTCCCAACTGACCCCGGGGACATAGCACCCTAGCCCCCTACAAAGGACTAG
                                                                                                                                                                                                                                                                                           509 CCACCCTCACTCGGCTCCATGAGGTCTCAGCCCCAAAACCCTACTAACTGTTGGATGTGCC
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/db_xref="taxon:9606"
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/organism="Homo
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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/mol type="mRNA"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE012XU24"
/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ScoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
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BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 9106 EVRY was constructed by Life Technologies, a
Givision of Invitrogen.
This sequence cluster 4215.r
For more information about this cluster, see
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8=CS0BAB011ZH12_AB01057_1&c=4215.r
                                                                                                                                  DA4U9304 11near EST 03-MAY-2004
BX409304 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE012YJ24
5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 TTACTGTTCTTTACCCCCTTTCGCTCTCACTGCACCCCCTCCATGCTGCTGTACAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
1 (bases 1 to 792)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2001 this sequence version replaced gi:30766967.
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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88.0%; Pred. No. 5.4e-153;
iive 0; Mismatches 82;
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                                                                                                                                                                                                                                           BX409304.2 GI:46956516
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ba84f03.y1 NIH MGC 21 Homo sapiens cDNA clone IMAGE:2907101 5'
similar to TR:095244 O95244 ENVELOPE PROTEIN ; contains Alu repetitive element;, mRNA sequence.

BE019603.1 GI:8279682
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                                             Gaps
                                            11;
                        814;
                       Length
                                             Indels
                       Score 537.6; DB 5;
Pred. No. 1.4e-147;
                                            0; Mismatches 105;
                      36.3%;
ilarity 85.3%;
Conservative
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                                 Similarity
                                            671;
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Best Local S:
Matches 671
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Homo sapiens (human)

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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:2907101"
/tlssue_type="choriocarcinoma"
/tlssue_type="choriocarcinoma"
/tlssue_type="choriocarcinoma"
/tlssue_type="choriocarcinoma"
/tlsp host="mblids (phage-resistant)"
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/note="organ: placenta; Vector: poTB7; Site_1: Xho1;
/note="organ: placenta; Vector: poTB7; Site_1: New York organ: placenta; Vector: placenta; New York of Callifornia, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Vertebrata; Euteleostomi;
                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing Cent
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primar: -40RP from Gibco
High quality sequence stop: 519.
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                                                             1 (bases 1 to 586)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Chordata; Craniata; Vertebrata; Butele
Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
   Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 586)
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Homo sapiens (nondara; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 760)

25 1i, W.B., Gruber, C., Jessee, J. and Polayes, D.

Rull-length cDNA libraries and normalization

10 may 22, 2003 this sequence version replaced gi:31018916.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web is www.genoscope.cns.fr

Ist sirand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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BX450495
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                                                                                                                                                                      241 GGAGTGCTAGGTGCACTAGGTACTGGCGGTATCACAACCTCTACTAGTTCTAC 300
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For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSOAU006ZG02_U0495_1&c=4215.r.

Location/Qualifiers
                                                                                                                                          GGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATCACAACCTCTACTCAGTTCTAC
                                                                                                                                                                                                                                                                          1042 TACAAACTATCTCAAGAAATAAATGGTGACATGGAACAGGTCACTGACTCCCTGGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
mol_type="maXN"
db_xref="taxon:9606"
/clone="CS0DE013XI20"
/tissue_type="PLACENTA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E I (bases I to 790)

In The Companies of Health, Mammalian Gene Collection (MGC)

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCM1576 row: c column: 23

High quality sequence stop: 624.
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/do_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4720846"
/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC."
/clone_lib="NIH MGC."
/clone_ib="NIH MGC."
/c
                                                                                                                                                                                                                                                                                                                                                                          BG572445 179 homo sapiens cDNA linear EST 10-APR-2001 602593490F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4720846 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.-ATTCTAGAGGCGGCGACGACGTG-dT (30) BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTCCCAATGCATCAGGTGAGGTAACACCTCCCACACGAATAGTCTGCCTACCCTCAGGA
                                                                   AACTCCCAATGCATCAGGTGGGTAACTCCTCCCACACAATAGTCTGCCTACCCTCAGGA
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                                                                                                                                   ACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAG 1288
                                                                                                                                                                      541 ACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAACGTAGAGCAG 586
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BG572445.1 GI:13580098
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Homo sapiens
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us-09-319-156b-9.rst

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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    917 ACAATCATGTGGTACCTAAGCCCCACAAAAAGAGTACCCAATTCTTCCTTTGTTATCA 976
                                                                                                                                                                                                                                                                                          AGAAATAGTGGTTGTGAGGCTCCTCAGCCAACGTAGTATGAAGGGCTCTTCAGAAAA 548
                                                                                                                                                                                                                                                                                                                       858 TATGTGCTCTCTCATTCTTAGTGCCCCCTATGACCATCTACACTGAAC-AAGATTTAT 916
                                                                                                                                                                                                                                                                                                                                        488 CCCATTAIGICATAICTAAGCCCAGCAACAAAAAGCICCCATTAIGTTAIAAG 429
                                                                                                                                                             GAAATAACCCATACCTCAAACCTGTGTGTAAAATTTAGCAATACT-ATAGACACAAC 740
                                                                                                                                                                                                                 CAGCICCCAAIGCAICAG---GIGGGIAACACCCICCCACACACAAIAGICIGCCIACCCIC 797
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                                                                                                           Length 760
                                                                                                          32.3%; Score 478.6; DB 5; Length 83.3%; Pred. No. 4.3e-130; ive 0; Mismatches 114; Indels
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Best Local Similarity 83.3
Matches 604; Conservative
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Search completed: January 22, 2005, 19:31:41 Job time : 4420.62 secs

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The present sequence represents a multiple sclerosis (MS) associated retrovirus (MSRV) protein used in the method of the invention. The invention provides complete or partial genomic sequences of the MSRV-1 pol gene, gag gene and env gene, and polypeptides encoded by these genes. The invention also provides antibodies raised against the polypeptides the MSRV-1 he genomic sequences, polypeptides and antibodies are also claimed useful for diagnosing infection by MS and rheumatoid architisa-associated viruses, and also for prevention and treatment of infection with these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid from retroviruses - useful for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 185-187; 286pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of, e.g. multiple sclerosis.
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N-PSDB; AAV43217.
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Komurian-Pradel F,
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Misc-difference
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Protein #
                                                       ; Search time 114 Seconds (without alignments) 1551.347 Million cell updates/sec
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                                                                                                               1 MALPYHTFLFTVLLPPFALT......KFVSSRIEAVKLQMVLQMEP
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ALIGNMENTS

Multiple sclerosis associated retrovirus; MSRV; MS; pol gene; gag gene; env gene; rheumatoid arthritis-associated virus. Ω Ω Multiple sclerosis associated retrovirus protein 3. , Bedin F, Paranhos-Baccala Jolivet-Reynaud C, Mandrand Multiple sclerosis associated retrovirus /note= "Encoded by tga" Location/Qualifiers Ş AAW71068 standard; protein; 493 97WO-IB001482 96US-00756429 entry)

- associated with

SXC

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This sequence represents the protein encoded by clone C15 from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                     SNTIDTTSSOCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIY
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                                                                      Nucleic acid sequences of retrovirus called MSRV-1 multiple sclerosis or rheumatoid polyarthritis.
                                                                                                                                                                                                                                                   99.9%; Score 2632; DB 2; L 100.0%; Pred. No. 4.5e-229; ive 0; Mismatches 0;
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                                                                                                               Claim 2; Page 38-39; 83pp; French
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Best Local Similarity 100.
Matches 493; Conservative
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                                     WPI; 1999-098275/09.
           BIO MERIEUX
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                                                 N-PSDB; AAX29703
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                                                                                                                   MALPYHTFLPTVLLPPFALTAPPPCCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSKGNS
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                                                   Length 493;
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                                                   Score 2632; DB 2; I
Pred. No. 4.5e-229;
                                           99.94; Scor.
100.04; Pred. No. ....
0; Mismatches
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Best Local Similarity
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Misc-difference
                           Sequence 493 AA;
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27-AUG-2003
08-JUN-1999
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The present sequence is encoded by a nucleotide sequence corressponding to the 3' env region and long terminal repeat sequences from clone CL6 of Multiple SCIENCESTE retrovirus (MSRV-1). The specification describes a long terminal repeat (LTR)-RUS region which encodes the expression of a MSRV-1 protein. This is unusual for LTRs, in particular in the RUS region. Probes and antibodies to the MSRV-1 retrovirus protein and encoding polynucleotide sequences are used to detect the presence of MSRV-1 retrovirus in a biological sample. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide fragment of LTR-RU5 region from Multiple Sclerosis retrovirus (MSRV) used to detect the presence of MSRV-1 retrovirus in a biological
                                                                                                                                                                               MSRV-1; pol region; long terminal repeat; LTR; RU5 region; retrovirus.
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/note= "N-linked glycosylation site"
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/note= "N-linked glycosylation site"
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280. .282
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Pred. No. 3.7e-228;
0; Mismatches 0; ]
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/note= "putative cleavage site"
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/note= "signal peptide<sup>r</sup>
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                                           AAB08195 standard; protein; 541
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Best Local Similarity 99.8%;
Matches 492; Conservative (
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04-DEC-2000
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                                                                                                                                                                                                                                                                      the pol gene of a treating multiple
                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid which comprises the gene of a retrovirus associated with multiple sclerosis or rheumatoid-arthritis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis. The present sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFTAHTHMPRICYNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTSMSDGGGI
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                                                                                                                                                                                                            Garson JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                   New isolated nucleic acid and their fragments having retrovirus, useful for diagnosing, preventing and/or sclerosis and/or rheumatoid arthritis.
                                                                                                                                                                                                ຕູ່ ຫຼ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.9%; Score 2632; DB 8; I
Best Local Similarity 100.0%; Pred. No. 4.5e-229;
Matches 493; Conservative 0; Mismatches 0;
                                                                                                                                                                                              Bedin F, Paranhos-Baccala
Jolivet-Reynaud C, Mandrand
                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 106; 193pp; English
Multiple sclerosis associated retrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the invention
                                                                                                                   96US-00756429.
97US-00979847.
                                                                                       03-APR-2002; 2002US-00114104
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                                                                                                                                                                                             Вевеше F,
                                                                                                                                                                                                                                         WPI; 2004-032461/03.
                                                                                                                                                              (INMR ) BIO MERIEUX
                                                                                                                                                                                                            Komurian-Pradel F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 493 AA;
                             US2003198647-A1
                                                                                                                   26-NOV-1996;
26-NOV-1997;
                                                         23-OCT-2003
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envelope protein expressed by the endogenous human retrovirus MRSV-1 has superantigen activity associated with autoimmune disease. The protien can be detected using the method of the invention. The specification describes a process for detecting activity of a superantigen in a biological sample. The process comprises identifying large scale expansion or loss of lymphocytes that carry at least one of the Vbetal6 expansion of loss of lymphocytes that carry at least one of the Vbetal6 inhibit the superantigen, especially those associated with MRSV-1 which is implicated in autoimmune disease, particularly multiple sclerosis. These agents are potentially useful for treatment or prevention (e.g. as vaccines), of autoimmune diseases
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          an envelope protein of MSRV-1. The
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                                                                                                                                                                                                                      Length 542;
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                                                                                                                                                                                                                   Score 2613; DB 3;
Pred. No. 2.7e-227;
2; Mismatches 4;
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transcriptase; ribonuclease H.
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98.8%;
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                                                                                                                                                                                                                                      Best Local Similarity 98.8
Matches 487; Conservative
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                                                                                                                                                                                             Sequence 542 AA;
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                                                                                                                                                                                                                                                                                                                                                     QNPTNCMMCLPLHFRPYISIPVPEQMNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKF
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                    MALPYHTFLFTVLLEPPFALTAPPPCCCTTSSSPYQEFL-RTRLPGNIDAPSYRSLSKGNS
                                                                         TETAHTHMPRINCYNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTSMSDGGGI
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                                                       TFTAHTHMPRNCYNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTSMSDGGGI
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Vbeta17; multiple sclerosis; vaccine.
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99FR-00013755.
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N-PSDB; AAA96625.
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28-OCT-1999;
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                     ONPINCWMCLPLHFRPYISIPVPEGWNXFSTEINTTSVLVGPLVSNLEITHTSNLTCVKF 240
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/note= "ENV polyprotein (coat polyprotein) domain"
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263. .484
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated or purified nucleic acid from a virus associated with multiple sclerosis and/or rheumatoid arthritis, anlipible sclerosis associated with multiple sclerosis and/or rheumatoid arthritis, pol, gag or reverse transcriptase genes (or their fragments) encoding the proteins or defined peptides (including immunodominant peptides, conserved motifs). Also included are a process for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample, a nucleic acid probe for the detection of a virus associated with multiple sclerosis or rheumatoid arthritis, a primer for the amplification by polymerisation of a nucleic acid of a viral material associated with multiple sclerosis or rheumatoid arthritis, a polymeptide exhibiting an inhibitory activity on the proteolytic, reverse transcriptase or ribonuclease H activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by immunogenic agent consisting of the antigenic polypeptide defined above. The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis, or for detecting in a biological sample, the presence of or exposure to a virus associated with multiple sclerosis or rheumatoid arthritis. The present sequence is a claimed MSRV-ample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accurately determined. Note: The SEQ ID numbers for the sequences as displayed in the main body of the patent do not match the SEQ ID numbers in the sequence listing. Consequently those sequences mentioned in the
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Pred. No. 1.3e-226;
3; Mismatches 3;
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                                                           97US-00979847
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KOMURIAN-PRADEL F.
JOLIVET-REYNAUD C.
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GARSON J A.
TUKE P W.
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Komurian-Pradel F,
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les 487; Conserv
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BESEME F.
                                                                                                                                                                                   BEDIN F.
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                                                           26-NOV-1997;
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(GARS/)
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endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory disorder such as acquired immune deficiency syndrome (AIDS), allergies, contact dermatitis, disorders of the placents such as preclampsia, abruptio placentes etc. Sequences of the invention are also useful for analysing a proteome of a tissue or a cell type. EMBRY proteins are useful as immunogens for preparing antibodies. Polynucleotides of the invention are useful for creating antibodies. Polynucleotides of the animals to model human diseases. They are also used in gene therapy. The present sequence is human EMBRY-2 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TFTAHTHMPRNCYNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTSMSDGGGI 120
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relates to human embryogenesis associated proteins (EMBRY)
                  and nucleic acid molecules encoding such proteins. EMBRY sequences are useful for screening modulators useful for treating or preventing disorders associated with abnormal expression of EMBRY. The disorders treated include reproductive disorders such as infertility,
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Pred. No. 2.9e-212;
8; Mismatches 26;
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ilarity 93.1%;
Conservative
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Best Local Simil
Matches 459; C
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This invention describes novel human secreted proteins encoded by polynucleotides isolated from human adult testes, adult brain, adult blood or adult placenta, or murine adult bone marrow or thymus cDNA libraries. The products of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, haemacopoiesis regulating activity, tissue growth activity, activity, activity, chemotactic/chemokinetic activity, haemostatic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for
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cadherin; tumour invasion suppressor; gene therapy; tissue growth
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88.6%; Pred. No. 1.1e-200;
ive 18; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 14a; Page 101-103; 142pp; English.
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N-PSDB; AAX77526.
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Best Local Similarity
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88.6%; Pred. No. 1.1e-200;

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IRDRIQCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRI
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Merberg D, Mi S, Treacy M;
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                                                    1 MALPYHIFLFTVLLPSFTLTAPPPCRCMTSSSPYQEFLWRMQRPGNIDAPSYRSLSKGTP
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                               1 MALPYHTFLFTVLLPPFALTAPPPCCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSKGNS
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Indels
18; Mismatches
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N-PSDB; AAD24195.
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immune disorder; severe combined immunodeficiency; SCID; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; allergic reaction; asthma; myeloid cell deficiency; lymphoid cell deficiency; osteoporosis; osteoarthritis;
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                                                                      The invention relates to identifying compounds which are modulators of syncytin expression. The syncytin modulators are useful in diagnosis and treatment of preedlampsia and gestational trophoblast disorders (e.g. choriocarcinoma, hydatiform mole, placental site tumour and missed/incomplete abortion). Syncytin is a human gene derived from the envelope gene of human endogenous defective retrovirus, HRRV-W. The present invention is based partly on the discovery that syncytin expression is dramatically reduced in preeclampsia, and is also mis-localised to the apical syncyticitophoblast membrane. The present sequence is human
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of syncytin in the cell is modulated in the presence of a test
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                                              Disclosure, Page 42-43; 43pp; English
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peripheral nervous system disease; peripheral neuropathy; Alzheimer's disease; Parkinson's disease; coagulation disorder; inflammatory response syndrome; SIRS; ischaemia-reperfusion injury; Crohn's disease; anaphylaxis; hypersensitivity; regeneration; neural cell proliferation; fertility; tumour; chemokine; human; secreted protein.
                                                                                             95US-00514014.
96US-006281364.
96US-00659221.
96US-00664596.
96US-00686878.
96US-00721148.
96US-00721148.
96US-00721148.
96US-00721192.
96US-00731318.
96US-00731318.
97US-00831382.
                                                                                  2002US-00114893
                                                         US2002193567-A1.
                                              Homo sapiens.
                                                                                  02-APR-2002;
                                                                                                                       17-JUN-1996
                                                                                                                                               27-SEP-1996;
                                                                                                                                                                                                             06-OCT-1999
                                                                     19-DEC-2002
                                                                                                                                                                  27-SEP-1996
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30-OCT-1996
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Collins-Racie LA, Evans C; Spaulding V, Carlin-Duckett Lavallie ER, Bowman MR, Treacy M, Mccoy JM, Jacobs K, Merberg D, Kelleher K;

(GEMY) GENETICS INST INC.

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WPI; 2003-657236/62. N-PSDB; ADC38776 Proteins AZ3021 encoded by clone AZ3021 from human adult colon, and BD12716 encoded by clone BD12716 from human fetal kidney cDNA library, useful for treating e.g. multiple sclerosis and rheumatoid arthritis.

Disclosure; SEQ ID NO 135; 412pp; English

The invention relates to a protein comprising fully defined A2302 1

Crotein or BD127 1 6 protein. The polymucleotides are useful for expressing recombinant proteins for analysis and are also useful as expressing recombinant proteins for analysis and are also useful as chromosome markers or tags to identify chromosomes or to map related gene continuous. The proteins are useful as amino acid supplement, carbon condined immunodeficiency (SCID), autoimmune disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. severe sclerosis, systemic lupus erythematosus, rhemmatoid arthritis, allergic creations (e.g. asthma), mysolid or lymphoid cell deficiencies, osteoporosis or osteoparthitis, peripheral nervous system diseases (e.g. peripheral neuropathy, Alzheimer's disease, Parkinson's disease), cospelation disorders, inflammatory diseases, Parkinson's disease), cresponse syndrome (SIRS), ischaemia-reperfusion injury, Crohn's disease), anaphylaxis and hypersensitivity. Proteins are also useful for inducing tumour immunity, for inducing bone, cartilage, tendon, ligament and/or nerve growth or regeneration for proliferating neural cells and for cregenerating nerve and brain tissue, for inducing fertility and for inducing are also useful as chemokine for inducing are indibiting tumour growth. Proteins are also useful as of emotine for inducing are indibiting tumour growth. Proteins are also useful as of emotine for inducing are also useful as chemokine for inducing are also useful so the proteins are also useful as chemokine for inducing are also useful as chemokine for inducing are also useful as chemokine for inducing are also useful as chemokine for inducing are also useful as chemokine for inducing are also useful as chemokine for analyses. mammalian cells (e.g., monocytes, fibroblasts, neutrophils), and also useful as inhibitors of receptor/ligand interactions. The present sequence represents the amino acid sequence of a human secreted protein.

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                                                                                                                                     ODQAREKHVKEVISQLTRVHGTSSPYKGLDLSKLHETLRTHTRLVSLFNTTLTGLHEVSA 180
                                                                                                                                                                                                           SNTTYTINSQCIRWVIPPIQIVCLPSGIFFVCGTSAYRCLNGSSESMCFLSFLVPPMTIY 300
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                                                            TFTAHTHMPRNCYNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTSMSDGGGI
                                                                                              TFTAHTHMPRICYHSATLCMHANTHYWTGKMINPSCPGGLGVTVCWTYFTQTGMSDGGGV
                                                                                                                                                                  ONPINCMICLPLNFRPYVSIPVPEQMNNFSTEINTISVLVGPLVSNLEITHISNLTCVKF
                                                                                                                                                                                                                                                                        1 MALPYHTFLFTVLLPPFALTAPPPCCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSKGNS
                                                                                                                                                                                          SNTIDTTSSQCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIY
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                                                                                                                                                                                                                                                               VTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSR1VTEKVKE
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                                                                                                                                                        ONPTINCHMCLPLHFRPYISIPVPEQWINFSTEINTTSVLVGPLVSNLEITHTSNLTCVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein;
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           envelope protein; multiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective;
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              Length 538;
                                 38; Indels
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/label= SU
/note= "surface protein"
317. .318
/note= "SU-TM putative cleavage site"
318. .538
/label= TM
/note= "transmembrane subunit"
               88.0%; Score 2319; DB 7;
88.6%; Pred. No. 1.1e-200;
ive 18; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisense-therapy; autoimmune disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human endogenous retrovirus
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                                                                                                                                                                                                                                                                                                                                                 EAVKLQMEPKMQ 492
                                Matches 436; Conservative
                         Best Local Similarity
Sequence 538 AA;
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con the basis of the PBS t-RNA motif used for the classification of human candogenous retrovirus (HERVs) the full length endogenous provirus which endogenous retrovirus (HERVs) the full length endogenous provirus which case he located on the long arm of human chromosome 7 (7q21-22) has been designated HERV-W. The present invention describes proteins or peptides (I) having superantigen (SAg) activity comprising the ENV protein (ENV) (CC of HERV-W, the surface protein (SU) and transmembrane (TM) sub-units. (I) have neuroprotective activity, and can be used in: vaccines; antisensetherapy; and HERV-W SAG activity-inhibitors. (I) and encoding DNA/RNA are therapy; and HERV-W SAG activity-inhibitors. (I) and encoding DNA/RNA are covering) capable of binding to a retroviral superantigen associated with MS; substances capable of blocking SAg activity and substances capable of blocking sagard from (I), modified to be capable of blocking transcription or translation of HERV-W retroviral SAG activity and being capable of generating an immune response against HERV-W retroviral SAG activity, capable of binding to a retroviral capable of blocking SAg activity, capable of binding transcription or translation of HERV-W retroviral superantigen associated with MS; or capable of binding transcription or translation of HERV-W retroviral superantigen for use in treating or preventing MS; obtained using (I) are useful for the treatment and preventing of MS. (I) and nucleic acide sequence represents the capable of binding them are useful for diagnosing autoimmune disease. The present sequence represents the capable of preventing of machine envolue of HERV-W present sequence represents the capable of binding them are useful for specifically claimed envelope protein of HERV-W designated G specifically claimed envelope protein of HERV-W designated G
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                                                                                                                                                                                                                                                                                                                                                       New human retrovirus HERV-W ENV proteins/peptides having superantigen activity useful for diagnosing and treating multiple sclerosis.
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88.4%; Pred. No. 3.2e-200;
iive 19; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 7; 94pp; English.
99EP-00402690
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Best Local Similarity
                                                                                                                                                                                                                                          WPI; 2001-316336/33
                                                                           UYGE-) UNIV GENEVE
                                                                                                                                                          Conrad B, Mach B;
                                                                                                                                                                                                                                                                                        N-PSDB; AAH20070
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The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immune response, e.g. in immunotherapy. HERV-7q peptides and their coding
                                                                                                                                                                                                                                                                                                                               301 TEQDLYNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid sequences of human endogenous retrovirus, HERV-7g, usdiagnosis, treatment and prevention of autoimmune and neurological
                                                                          361 VADSLVTLQDQLNSLAAVVLQNRRALDLLTAERGGTCLFLGEECCYYVNQSGIVTEKVKE
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                                                QGQAREKQVKEAISQLTRGHSTPSPYKGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human retroviral HERV-7q env peptide #3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human endogenous retrovirus envelope protein. The specification describes a method for detecting expression of an envelope protein from a human endogenous retrovirus (HERV), in cells, of a tissue or culture. The method comprises detecting syncytia formation due to the fusogenic properties of the envelope protein. Envelope prophylactic compositions, particularly for treatment of cancer, to correct defects in placental development (or other natural formation of ther types of syncytia), and to promote adhesion of cells in grafts or cellular repair processes. Expression of sequences antisense to the polynucleotide are used to prevent formation of syncytia
VADSLVTLQDQLNSLAAVVLQNRRALDLLTAERGGTCLFLGEECCYYVNQSGIVTEKVKE 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting expression of human endogenous retrovirus envelope protein in cells of a tissue or culture, from its ability to induce syncytia.
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                                                                        IRDRIQCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLFGPCIFNLLVKFVSSRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruggieri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Envelope protein; HERV; syncytia formation; placental development;
syncytia; cancer; cell adhesion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blond J, Lavillette D,
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(INRM ) INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                 AAB67652 standard; protein; 538 AA
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sequences can be used in immunogenic or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                      QDQAREKHVKEVISQLTRVHGTSSPYKGLDLSKLHETLRTHTRLVSLFNTTLTGLHEVSA 182
                                                                                                                                                                                                                                                                242
                                                                                                                                                                                                                                                                                    300
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                                                                                                                             1 MALPYHTFLFTVLLPPFALTAPPPCCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSKGNS 60
                                                                                                                                                                            TFTAHTHMPRINCYHSATLCMHANTHYWTGKMINDSCPGGLGVTVCWTYFTQTGMSDGGGV
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                                                                                                                                        MALPYHIFLFTVLLPSFTLTADPPCRCMTSSSPYQEFLWRWQRPGNIDAPSYRSLSKGTP
                                                                                                                                                                                                                                              ONPTINCHMCLPLHFRPYISI PVPEQMNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKF
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                                                                                      540;
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                                                                                                         38; Indels
                                                                                      Length
                                                                                     ; Score 2314; DB 3;
; Pred. No. 3.2e-200;
19; Mismatches 38;
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                                                                                      87.9%;
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The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q.
Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immune response, e.g. in immunocherapy. HERV-7q peptides and their coding sequences can be used in immunocherapy. HERV-7q peptides and their coding sequences can be used in immunocherapy. HERV-7q peptides and their coding protection against autoimmune diseases, particularly multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ODQAREKHVKEVISQLTRVHGTSSPYKGLDLSKLHETLRTHTRLVSLFNTTLTGLHEVSA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNPTNCWICLPINFRPYVSIPVPEQMNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKF 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEQDLYNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQ 360
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                                                                                                                                                                           nucleic acid sequences of human endogenous retrovirus, HERV-7q, used diagnosis, treatment and prevention of autoimmune and neurological
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88.4%; Pred. No. 4.5e-200;
iive 19; Mismatches 38;
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                         Claim 22; Page 152-154; 225pp; French
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                                                          Perin J,
                                                                                                                    WPI; 2000-160587/14
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Best Local Similarity
Matches 435; Conserv
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591 TEQDLYSYVISKPRNKRVPILPFVIGAGVLGALGTGIGGITTSTQFYYKLSQELNGDMER
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2001US-0339453P.
2002US-0365091P.
2002US-0365384P.
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2002US-00128558
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                                                                                                                                      EAVKLOMEPKMO 782
                                                                                                                     EAVKLOMVLOME 492
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                                                                                                                                                                                                                                                                                                                                                            WO2003054152-A2.
                                                                                                                                                                                                                                                                                                                                      Unidentified.
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11-DEC-2001;
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14-MAR-2002;
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Ghosh M,
Ma Y, War
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                        361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEQDLYNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQPYYKLSQEINGDMEQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 MALPYHIFLFTVLLPSFTLTAPPPCRCMTSSSPYQEFLWRMQRPGNIDAPSYRSLSKGTP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFTAHTHMPRNCYNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTSMSDGGGI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFTAHTHMPRNCYHSATLCMHANTHYWTGKMINPSCPGGLGVTVCWTYFTQTGMSDGGGV 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGQAREKQVKEAISQLTRGHSTPSPYKGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNTIDITSSQCIRWVIPPIRIVCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMIIY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid sequences of human endogenous retrovirus, HERV-7g, used for diagnosis, treatment and prevention of autoimmune and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MALPYHTFLFTVLLPPFALTAPPPCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSKGNS
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                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to new nucleic acid sequences of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 846;
                                                                       chromosome 7q; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.9%; Score 2314; DB 3;
88.4%; Pred. No. 6.1e-200;
ive 19; Mismatches 38;
                                                                                                                                                                                                                              (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                 Example 4; Fig 19; 225pp; French
                                                                                                                                                                                                                                                     Rieger F;
                                                                                                                                                                                                       98FR-00007920.
                                                                       HERV-7q;
                                                                                                                                                                                99WO-FR001513
                                                                                                            Human endogenous retrovirus.
                        (first entry)
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435; Conservative
                                                 HERV-7g env protein #1
                                                                                                                                                                                                                                                     Alliel PM, Perin J,
                                                                       disease;
                                                                                                                                                                                                                                                                           WPI; 2000-160587/14.
                                                                                    multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 846 AA;
                                                                                                                                 WO9967395-A1
                                                                                                                                                                                23-JUN-1999;
                                                                                                                                                                                                        23-JUN-1998;
                        01-AUG-2002
                                                                                                                                                        29-DEC-1999
                                                                         Autoimmune
   ABP41050;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang J;
Wang Z;
                            VTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKE
                                                                                                               IRDRIQCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder; contig.
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ou P, Drmanac RT,
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88.6%; Pred. No. 1e-199;
iive 19; Mismatches 36;

    Ren F, Zhang
leng G, Zhou P,
Boyle BJ;

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4, Xue AJ, Wehrman T, Wer
Wang D, Chen R, Xu C, Bo
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The present invention describes isolated polynucleotide sequences (1), which encode polypeptides (11) with biological activity. Also described:
(11) a vector comprising (1); (2) an expression vector comprising (1); (3)
a host cell genetically engineered to comprise (1) which is operatively associated with a regulatory sequence that modulates expression of (1) in the host cell; (4) a polypeptide (II) encoded by (1); (5) a composition comprising the polypeptide of (4) and a carrier; (6) an antibody directed against the polypeptide of (4) and a carrier; (6) an antibody directed against the polypeptide of (4); (7) detecting (1) or the polypeptide of (4) in a sample; (8) identifying a compound that binds to the polypeptide of (4) in a semple; (9) producing the polypeptide of (4); and (10) a collection of polymucleotides comprising at least one of the polymucleotide sequences (1). The polynucleotides (1) can be used as hybridisation probes, (1). The polymucleotides (1) can be used as hybridisation probes, coligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA. The present sequence represents a human contig polypeptide sequence, which is used in an example from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNTTYTHNSQCIRWVTPPTQIVCLPSGIFFVCGTSAYRCLNGSSESMCFLSFLVPPMTIX 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biological activity, genetic engineering, hybridisation probe, oligomer,
primer; chromosome mapping; gene mapping; recombinant protein production;
                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides, useful as hybridization probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA.
                                                                                                             MALPYHIFLFTVLLPSFTLTAPPPCRCMTSSSPYQEFLWRWQRPGNIDAPSYRSLSKGTP
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                                                    MALPYHTFLFTVLLPPFALTAPPPCCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSKGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ONPTINCHMCLPLHFRPYISIPVPEQWINFSTEINTTSVLVGPLVSNLEITHTSNLTCVKF
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The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CWWCLPLHFRPYISIPIPEQWNNFSTEINTTSVLVGPL-SNLEITHTSNLTCVKFSNTID 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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                                                                                                                                                                                              Peptide #4442 encoded by probe for measuring cervical gene expression.
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                                                                                                                                                                                                                              human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.9%; Score 1235.5; DB 4; Length 89.4%; Pred. No. 5.1e-103; Live 8; Mismatches 19; Indels
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                                                                                                       AAM18008 standard; protein; 263 AA.
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Best Local Similarity
Matches 236; Conserv
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03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                            New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the open reading frame 1 encoding the envergence in the human endogenous retrovirus (HERV) W (AAX25665). Nucleic cacids, their fragments or peptides encoded by them derived from the HERV-W genome are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulindependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes associated with this susceptibility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEQDLYNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIDSLVILODOLNSLAAVVLQNRRALDLLIAKRGGICLFLGEERCYYVNOSRIVIEKVKE 420
 polyarthritis; insulin-dependent diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGLPYHIFLCSVLSPCFTLTAPPPCRCMTSSSPHPEFLWRWQRPGNIDAPSYRSLSKGTP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNPTNCWICLPLNFRPYVSIPVPEQWNNFSTEINTTSVLVGPLVSNVEITHTSNLTCVKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MALPYHTFLFTVLLPPFALTAPPPCCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSKGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFTAHTHMPRNCYNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTSMSDGGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
multiple sclerosis; rheumatoid polyarthritis; insulin-dependent
disseminated lupus erythematosus; pregnancy; chromosomal marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.9%; Score 2237; DB 2; Length 538;
85.6%; Pred. No. 3e-193;
.ive 26; Mismatches 45; Indels (
                                                                                                                                                                                                                                 Mallet
                                                                                                                                                                                                                                 Mandrand B,
                                                                                                                                                                                                                                                                                                                                                         Example 8; Fig 6; 106pp; French
                                                                                                                                                                                                                                   Bouton O,
                                                                                                                                       98WO-FR001442.
                                                                                                                                                                      97FR-00008815
                                               endogenous retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                              WPI; 1999-120897/10.
                                                                                                                                                                                                                                   Blond J,
                                                                                                                                                                                                    (INMR ) BIO MERIEUX
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Matches 421; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 538, AA;
                                                                                                                                       06-JUL-1998;
                                                                                                                                                                      07-JUL-1997;
                                                                            WO9902696-A1
                                                                                                         21-JAN-1999
                                                                                                                                                                                                                                   Вевеше F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361
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TANSQCIRWVIPPTRIVCLPSGIFFVCGTSAYHCLNGSSESVCFLSFLVAPMPIYTEQDL 179
                                                                   365
                                                                                            180 YNHVIPKPRNKRVPILPFVIGAGVLGGVATGIGGITTSTQFYYKLSQELNGDMEWVADTL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #4556 encoded by probe for measuring placental gene expression.
                                                                 YNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKFSNTID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microarray, human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1235.5; DB 4;
Pred. No. 5.1e-103;
8; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 30788; 654pp; English.
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                                                                                                                                                       389
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                                                                                                                                                       VTLQDQLNSLAAVVLQNRRALDLL
                                                                                                                                                                              VILODOLNSLAAVVLONRRALDLL
                                                                                                                                                                                                                                                                                                             standard; protein; 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US000663
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Best Local Similarity 89.4%;
Matches 236; Conservative 8
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human genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                              17-0CT-2001
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                        120
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                                                                                                                                                                                                                                                                                                             AAM30519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe;
                                                                                                                                                                                                                                                                    RESULT 22
                                                                                                                                                                                                                                                                                          AAM30519
                                                                                                                                                                                                                                                                                                                               셤
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                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
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                        YNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSL 365
                                                 Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CWMCLPLHFRPYISIPIPEQWNNFSTEINTTSVLVGPL-SNLEITHTSNLTCVKFSNTID 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                            Peptide #4549 encoded by human foetal liver single exon probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 29678; 639pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1235.5; DB 4
Pred. No. 5.1e-103;
8; Mismatches 19;
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                                                                                                          VILODOLNSLAAVVLONRRALDLL 389
                                                                                                                                                     263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression in human fetal liver.
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                                                                                                                                   ABB37043 standard; peptide; 263
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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2000US-0207456P.
2000US-00608408.
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Best Local Similarity 89.4%;
Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157277-A2
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30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                        306
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Sequence 263 AA;

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expession in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from expension by the probes are useful for verifying the probes of the microarray. The probes are useful for verifying the propession of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring cannown acknown of the proposition of functional information from genomic sequence. The present sequence tag microarrays the method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed sequences:

The proposition but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                          YNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSL 365
TTSSQCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIYTEQDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                        Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                  Peptide #4463 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 14780; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
                                                                                                                                               VTLQDQLNSLAAVVLQNRRALDLL 389
                                                                                                                                                                    VILODOLNSLAAVVLONRRALDLL 263
                                                                                                                                                                                                                                                                            ABB31812 standard; peptide; 263 AA
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26-MAY-2000; 2000US-0201456P.
30-UIN-2000; 2000US-00608408.
21-SEP-2000; 2000US-0234667P.
21-SEP-2000; 2000US-0234667P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                    245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                 61 CWMCLPLHFRPYISIPIPEQWNNFSTEINTTSVLVGPL-SNLEITHTSNLTCVKFSNTID
                                                  126 EKQVKEAISQLTRGHSTPSPYKGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSAQNPTN
                                                                    | SKHIKEVISQLTWVHSTPGPYKGLDLSKLHETLHTHTGLVSLFNTTLTGLHEVSAQNPTN
                                                                                                    186 CWMCLPLHFRPYISIPVPEQWNNFSTEINTISVLVGPLVSNLEITHTSNLTCVKFSNTID
                                                                                                                                                     246 TISSOCIRWVIPPIRIVCLPSGIFFVCGISAYHCLNGSSESMCFLSFLVPPMTIYTEQDL
                         Gaps
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Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, gene expression, heart, microarray, vascular system;
cardiovascular disease, hypertension, cardiac arrhythmia;
                          Indels
 4;
                          19;
Score 1235.5; DB 4
Pred. No. 5.1e-103;
                         8; Mismatches
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                                                                                                                                                                                                                                                                         240 VILQDQLNSLAAVVLQNRRALDLL 263
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                                                                                                                                                                                                                                                                                                                                                   ABB22358 standard; protein; 263
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2000US-0234687P.
2000US-0236359P.
 46.9%;
89.4%;
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2000US-00608408
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                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
 Query Match 46.9
Best Local Similarity 89.4
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                congenital heart disease.
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27-SEP-2000;
04-OCT-2000;
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By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                     245
                                                                                                                                                                                                                                                                                                                                                                           CWACLPLHFRPYISIPIPEQWNNFSTEINTTSVLVGPL-SNLEITHTSNLTCVKFSNTID 119
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microarray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                                                                                                               Length 263;
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Pred. No. 5.1e-103;
8; Mismatches 19;
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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2000US-00608408.
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89.4%;
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Best Local Similarity 89.4
Matches 236; Conservative
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                          245
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Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human brains.
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English
                                                                                                                                                                                                                                                               4; Length
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4; SEQ ID NO 30491; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                 19;
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Pred. No. 5.1e-103;
8; Mismatches 19;
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26-MAY-2000; 2000US-0201456P.
30-UNA-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
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Best Local Similarity 89.4'
Matches 236; Conservative
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                                                                                                                                                                                                                  Sequence 263 AA;
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09-AUG-2001
                         Claim 27;
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Human
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                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
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                                                                                                                                                                                   CWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKFSNTID
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                                                                                                                                                                                                                                                       YNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSL
                                                                                                                                                  EKQVKEAISQLTRGHSTPSPYKGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSAQNPTN
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
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          SEQ ID NO 29875; 650pp + Sequence Listing; English.
                                                                                                               Length 263;
                                                                                                                                19; Indels
                                                                                                               DB 4;
                                                                                                              Score 1235.5; DB 4
Pred. No. 5.1e-103;
8; Mismatches 19;
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26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
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27-SEP-2000; 2000US-0236359P.
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                                                                                                               46.9%;
89.4%;
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                                                                                                              Query Match
Best Local Similarity 89.4
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Human liver peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
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                                                                                               Sequence 263 AA;
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          Example 4;
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measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nuclectide sequences given in the specification for complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59990 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245
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for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 EKQVKEAISQLTRGHSTPSPYKGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSAQNPTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                          The invention relates to a single exon nucleic acid probe (SENP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 263;
exon nucleic acid probes useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1235.5; DB 4
Pred. No. 5.1e-103;
8; Mismatches 19;
                                                                                            SEQ ID NO 30533; 658pp; English
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                                gene expression in human adult liver
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
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Best Local Similarity 89.4%;
Matches 236; Conservative
   genome-derived single
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Query Match
Best Local Similarity 89.4
Matches 236; Conservative
  The present invention relates to novel single exon nucleic acid probes (see AA100010-AA10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a predicting, diagnosing, grading, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CWMCLPLHFRPYISIPIPEQWNNFSTEINTTSVLVGPL-SNLEITHTSNLTCVKFSNTID 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TANSQCIRWUTPPTRIVCLPSGIFFVCGTSAYHCLNGSSESVCFLSFLVAPMPIYTEQDL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNHVI PKPRNKRVPI LPFVI GAGVI GGVATGI GGITTSTQFYYKLSQELNGDMEWVADTL 239
                                                                                                                   Novel single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKQVKEAISQLTRGHSTPSPYKGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSAQNPTN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKFSNTID 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSQCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIYTEQDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human peptide encoded by genome-derived single exon probe SEQ ID 29484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; single exon probe; asthma; lung cancer; COPD; ILD;
chronic Obstructive pulmonary disease; interstital lung disease;
familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                         ٦;
                                                                                                                                                                                                                                                                                                                                                                                            46.9%; Score 1235.5; DB 4; Length 263; 89.4%; Pred. No. 5.1e-103; ive 8; Mismatches 19; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                          Claim 27; SEQ ID NO 14388; 322pp; English.
                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTLQDQLNSLAAVVLQNRRALDLL 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG39819 standard; peptide; 263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 VTLQDQLNSLAAVVLQNRRALDLL
                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                 Chen W,
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 236; Conservative
                                                                 Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                         WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                       Sequence 263 AA;
                                                                                                                                  a human breast.
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ઠે 셤 ઠે ઠે

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample of the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) agorithmically predicting specific hybridisation of detectably continued and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, comprising (a) identifying exons from genomic sequences of in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon common pattern of microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the tissues and/or cell types using hybridisation to a single exon common general probes/open reading frames (ORF). The probes are used for general pung exons in a gene, a peptide comprising one cof 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for general for indentifying exons in a gene, particularly using human cancer, chronic obstructive p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon probe of
1 not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karaganer syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
                                                                                                                       Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    directly from WIPO at ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                      measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 29484; 634pp; English
WPI; 2002-114183/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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Chen W, Rank DR,

Penn SG, Hanzel DK,

(MOLE-) MOLECULAR DYNAMICS INC

2000US-00632366. 2000US-0234687P. 2000US-0236359P.

21-SEP-2000; 27-SEP-2000; 04-OCT-2000;

03-AUG-2000;

30-JUN-2000

04-FEB-2000;

2000GB-00024263

2000US-00608408

30-JAN-2001; 2001WO-US000665

hyaline membrane disease

WO200186003-A2 Homo sapiens.

15-NOV-2001

Gape

1;

Score 1235.5; DB 5; Length 263; Pred. No. 5.1e-103; 8; Mismatches 19; Indels 1:

46.9%;

Seguence 263 AA;

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245
                                                                              CWMCLPLHFRPYISIPIPEQWNNFSTEINTTSVLVGPL-SNLEITHTSNLTCVKFSNTID 119
                                                                                                                           305
                                                                                                                                            YNHVIPKPRNKRVPILPFVIGAGVLGGVATGIGGITTSTQFYYKLSQELNGDMEWVADTL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclecides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polymeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in
185
                                                                                                                                                                                           YNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II)
                            9
                    CWMCLPLHFRPY1S1PVPEQWNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKFSNT1D
                                                                                                                          TISSOCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIYTEQDL
EKOVKEAISOLTRGHSTPSPYKGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSAQNPTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 37891; 103pp; English.
                                                                                                                                                                                                                                                         VTLQDQLNSLAAVVLQNRRALDLL 389
                                                                                                                                                                                                                                                                             VILODOLNSLAAVVLONRRALDLL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #7523.
                                                                                                                                                                                                                                                                                                                                                                     ABG07532 standard; protein; 446 AA
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2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446
diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this spatent did not appear in the printed specification, but was obtained in the vipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                          116 IIPRCGLPRGL------OSD----NGPAFKATVTQGLSQMSDTSWEGRYPVIL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                       207 LFKQQPPHISIPVPEQWNNFSTEINTTSILVGPLVSNLEITHTSNLTRVKFSNTIDTTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 QCIRWYTPPIQIVCLPSGIFFVCGTSAYHCLNGFSESMCFLSFLVHPMTIYTEQDLYNYV
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                                                                                                                                                                                                                                                                                                                                                                               159 STPTAVKVAGVESRIH-----HTRVKPW-----LLPKEPGNPGDNASYSCEPLEDLGL
                                                                                                                                                                                                                                                                                                                                                                                                                      -FR---PYISIPVPEQWNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKFSNTIDTTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 QCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIYTEQDLYNHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 DQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRA
                                                                                                                                                                                                                                                                          ---RGH----
                                                                                                                                                                                                                                       51; Gaps
                                                                                                                                                                                                   4; Length 446;
                                                                                                                                                                                                                                                                        92 INPSC--PGGLGATVCWTYFTHTSMSDGGGLQGQAREKQVKEAISQLT
                                                                                                                                                                                                                                         41; Indels
                                                                                                                                                                                                   42.9%; Score 1130.5; DB 68.1%; Pred. No. 3.5e-93; ive 23; Mismatches 41
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le : 122 secs
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Matches 245; Conservative
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JS-08-979-847B-106
RESULT 1
 Sequence 106, App
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Sequence 2, Appli
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(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-691-5612-87
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US-08-91-5612-87
US-08-176-87
US-09-176-87
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US-09-116-09-14
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US-09-116-09-14
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US-09-116-09-14
US-09-116-09-16
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US-08-16-1074-117
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US-08-919-597-107
US-08-475-668A-107
US-08-485-551A-107
US-08-471-913A-107
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                                                                                                                                                                                                                                                                                                                                        478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB
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MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILLP
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
THERAPEUTIC PURPOSES
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ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/979, 847B
FILING DATE: 26-NO. 6582703-1997
FILING DATE: 26-NO. 6582703-1997
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-2787
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 antino acids
TYPE: amino acid
STRANDEDNESS: single
              US-08-474-349A-107
US-08-470-896-107
US-08-485-546A-107
US-08-485-546A-107
US-09-315-127-6
US-09-315-127-6
US-09-111-085-4
US-09-111-085-4
US-09-111-085-4
US-09-376-781-4
US-09-376-781-3
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Patent No. 6582703
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
BEDIN, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
COMURIAN-PRADEL, FLORENCE
COMURIAN-PRADEL, FLORENCE
COLLIVET-REYNAUD, COLETTE
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TOPOLGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-08-979-847B-106
                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRI
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
1922
1922
1922
1922
2322
6657
6657
6657
1931
1961
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STATE: VP
COUNTRY:
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US-08-007-282B-2
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APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: Lavalile, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Treacy, Maurice
APPLICANT: Mi, Sha
APPLICANT: AFERICANT: SECHETE PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION: SECHETE PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6006B.AJ172A
CURRENT APPLICATION: SECHETE PROTEINS
CURRENT FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
SSOFTWARE: S38
                                                                                                                                      TFTAHTHMPRNCYNSATLCMHANTHYWTGRMINPSCPGGLGATVCWTYFTHTSMSDGGGI 120
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                                                                             1 MALPYHTFLFTVLLPPFALTAPPPCCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSKGNS
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                                                            1 MALPYHTFLFTVLLPPFALTAPPPCCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSKGNS
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88.6%; Pred. No. 5.9e-230;
ive 18; Mismatches 38; Indels
 Length 493,
                              Indels
99.9%; Score 2632; DB 4; I 100.0%; Pred. No. 2.8e-262; iive 0; Mismatches 0;
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                              Matches 493; Conservative
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ORGANISM: Homo sapiens
              Similarity
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Matches 436
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Sequence 2, Application US/08007282B

Sequence 2, Application US/08007282B

Sequence 2, Application US/08007282B

GENERAL INFORMATION:
APPLICANT: WITTER, TRICHARD L.
APPLICANT: WITTER, TRICHARD L.
APPLICANT: YANAGIDA, NOBORD:
TITLE OF INVENTION: VACCINE COMPRISING FOWLPOX VIRUS
TITLE OF INVENTION: AVIAN RETICULOENDOTHELIOSIS RETROVIRUS
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 2
CORRESPONDENCES: 2
CORRESPONDENCES: 2
CORRESPONDENCES: 3
TREET: 8110 Gatehouse Road Suite 500 East
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                         300
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181 QNPINCWICLPLNFRPYVSIPVPEQWNNFSTEINTTSVLVGPLVGPLVSNLEITHTSNLTCVKF
                                                                                                               61 TFTAHTHMPRNCYHSATLCMHANTHYWTGKMINPSCPGGLGVTVCWTYFTQTGMSDGGGV
                                                                               TFTAHTHMPRNCYNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTSMSDGGGI
                                                                                                                                                                                                                                                                                         ONPINCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 VIDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartable
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,282B
FILING DATE: 19930121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1644-104P
TELECOMMUNICATION INFORMATION:
TELEPAK: 703-205-8000
TELEFAK: 703-205-8050
TELEFAK: 248345
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COMPUTER READABLE FORM:
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APPLICANT: Herve PERRON
APPLICANT: Frederic BESEME
APPLICANT: Frederic BESEME
APPLICANT: Frederic BEDIN
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: GOJETE O'OLIVET
APPLICANT: Bernard MANDRAND
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: THERAPEUTIC PURPOSES
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT)
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACTION OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCREEN OF THE SCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 162;
                          MEDIUM TYPE: Floppy disk
COMPUTER: IN PC Compatible
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY COMPATIBLE
COPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/979, 847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: GLIANOWA
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLILAM P.
REGISTRATION NUMBER: 30, 024
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.6%; Score 516; DB 4;
87.6%; Pred. No. 6.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/691,563C
FILING DATE: 02-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 87, Application US/08691563C Patent No. 6001987 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 162 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 109: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Berridge, William P. REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC (OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-979-847B-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-691-563C-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 THMPRNCYNSATLCMHANTHYWT------GKMINPSCPGGLGATVCWTYFT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 QTSDILBATHQVLNATNPKLABNCWLCMTL--GTPIPAAIPTNGNVTLDGNCSLSLPFGC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 NPPGSIDVSCYAGEADNRTGIPVG-----YVHFTNCTSIQ---EVTNETSQ----MGN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 LTRL-CPPPGHVFVCGNNMAYTALPNKWIGLCILASIVPDISIISGEE----PIPLPSIE 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 HTSMSDGGGIQGQAREKQVKEAISQLTRGHSTPS-PYKGLVLSKLHETLRTHTRLVSLFN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 PVYVSDGGGPTDMIREESVRERLEBIIR-HSYPSVQYHPLALPR------SRGVDLDP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TT---LTRLHEV-SAQNP---TNCWMCLPLHFRPYISIPVPEQWN-----NFSTEI---- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTRIVCLPSGIFFVCGTS-AYHCLNGSSESMCFLSFLVPPMTIYTEQDLYNHVVPKP--- 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HNKRVPILPFVIRAGVLGRL---GTGIGSITTSTQFYYKLSQEINGDMEQVTDSL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----NTTSVLVGPLVSNLEITHTSNLTCVKFSNTIDTTSSQCIRWVTP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 YTARRHKRAVQFIPLLVGLGISGATLAGGTGLG---VSVHTYHKLSNQLIEDVQALSGTI 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTLODOLNSLAAVVLONRRALDLLTAKRGGTCLFLGEERCYYVNOSRIVTEKVKEIRDRI 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508 IERKRALYDNPLWSGLNGFLPYLLPLIGPLFGLILFLTLGPCIMKTLTRIIHDKIQAVK 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         426 OCRAEELONTERWGLLSOWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRIEAVK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
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                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                      21.2%; Score 559.5; DB 1; Length 31.9%; Pred. No. 1.5e-48; rive 75; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VSA
COUNTRY: USA
ZIP: 22320
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BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KOMURIAN-PRADEL, FLORENCE
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GARSON, JEREMY
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BESEME, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOLIVET-REYNAUD,
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CORRESPONDENCE ADDRESS:
                              SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acids
TYPE: AMINO ACID
STRANDEDRESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 153; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
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US-08-979-847B-109
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA.
                                                                                                                                                                                                                                                                                                         66 GGLCTFLGBECCFYTNQSGIVRDATWHLQERASDIRQCLSNSYTN-----LWSWATWLL 119
                                                                                                                                                                                            334 GTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKR 393
                                                                                                                                                                                                                                                                                   394 GGTCLFLGEERCYYVNQSRIVTEKVKEIRDRI----QCRAEELQNTERWGLLSQWMPWVL 449
                                                                                                                                                                                                                        6 GTGIAGLSTSLSYYHTLSKNFSDSLQEIMKSILTLQSQLDSLAAMTLQNRRGPHLLTAEK 65
                                                                                                                                                 10; Gaps
                                                                                                        Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979, 847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                       450 PFLGPLAALILLLEGPCIFNLLVKFVSSRIEAVKLOMVLOMEP 493
                                                                                                                                                                                                                                                                                                                                                                                                  120 PFLGPMAAILLLLTFGPCIFKLLVKFVSSRIEAIKLQMVLQMEP 163
                                                                                                                                                 38; Indels
                                                                                                      17.2%; Score 452; DB 4; 54.3%; Pred. No. 1.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTATION UNDRER: 30,024
REPERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-787
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THERAPEUTIC PURPOSES
                                                                                                                                               27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BERRIDGE, PLC
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TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 81:
US-08-979-8478-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULY: /
US-08-979-847B-81
; Sequence 81, Application US/08979847B
; Patent No. 6582703
; GENERAL INFORMATION:
; APPLICANT: PERRON, HERVE
; APPLICANT: PERRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 433 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENČE ADDRESS:
ADDRESSEE: OLIFF & BERI
STREET: P.O. BOX 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUKE, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ALEXANDRIA STATE: VA
                                                                                                                                                 89; Conservative
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                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-374-766-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
amino acid
                                                                                                        Query Match
Best Local Similarity
Matches 89; Conserv
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APPLICANT: Frederic BEDIN
APPLICANT: Frederic BEDIN
APPLICANT: Frederic BEDIN
APPLICANT: Glaucia BEDIN
APPLICANT: Colette JOLIVEN
APPLICANT: Colette JOLIVEN
APPLICANT: Bernard MANDRAND
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: THERAPEUTIC PURPOSES
TITLE OF INVENTION: THERAPEUTIC PURPOSES
CORRESPONDENCES: 92
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 GGLCTFLGEECCFYINOSGIVRDATWHLOERASDIRQCLSNSYIN-----LWSWATWLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTCLFLGEERCYYVNQSRIVTEKVKEIRDRI----QCRAEELQNTERWGLLSQWMPWVL 449
                                                                                                                                                                                                                                                                                                                                                       334 GTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKR 393
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                         38; Indels 10;
                                                                                                                                                                                                                                                              DB 3; Length 433;
1.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFLGPMAAILLLTFGPCIFKLLVKFVSSRIEAIKLOMVLOMEP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFLGPLAALILLLFGPCIFNLLVKFVSSRIEAVKLQMVLQMEP 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Oliff & Berridge
700 South Washington Street, Suite 300
                                                                                                                                                                                                                                                                17.2%; Score 452; DB 54.3%; Pred. No. 1.2e-
ive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REPERENCE/DOCKET NUMBER: WPB 38588
TELECOMMUNICATION:
TELEPHONE: 703-836-6400
  REFERENCE/DOCKET NUMBER: WPB 38588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/374,766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 87, Application US/09374766 Patent No. 6579526
               TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEPRAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity 54.3%,
Best Local 80, Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                      TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-691-563C-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia COUNTRY: U.S.A. ZIP: 22314
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STREET: 70
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Sequence 3, Application US/09315127
Patent No. 6448390
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                              US-09-315-127-3
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                                    Gaps
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Sequence 2, Application US/09315127
Sequence 2, Application US/09315127
GENERAL INFORMATION:
APPLICANT: THE UNIVERSITY Of Tennessee, c/o Richard Cox
TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
FILE REFERENCE: 44137-5023, U. of Tennessee
CURRENT APPLICATION NUMBER: US/09/315,127
CURRENT PILIG DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
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Length 433;
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17.2%; Score 452; DB 4;
54.3%; Pred. No. 1.2e-37;
ive 27; Mismatches 38;
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                                    89; Conservative
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: The University of Tennessee, c/o Richard Cox TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy FILE REFERENCE: 44137-5023, U. of Tennessee CURRENT APPLICATION NUMBER: US/09/315,127 CURRENT FILING DATE: 1999-05-20 NUMBER OF SEQ ID NOS: 23 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 31 LENGTH: 632
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                                                                                                                                       448 VLPFLGPLAALILLLEGPCIFNLLVKFVSSRIEAVKLQMVLQ 490
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15.5%; Score 407.5; DB 4;
Best Local Similarity 25.0%; Pred. No. 8.5e-33;
Matches 146; Conservative 77; Mismatches 227;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                     APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
FILE REPERENCE: P50489
CURRENT APPLICATION NUMBER: US/09/309,572
CURRENT PILING DATE: 1999-05-11
EARLIER APPLICATION NUMBER: DE 198 56 463
EARLIER FILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 24
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578 ISTIMGPLIVLLMILLFGPCILNRLVQFVKDRISVVQALVLTQ
                                                                                                                                                                                                                                                                                                                                                                                       15.5%; Score 407.5; DB 4; 25.0%; Pred. No. 9.2e-33; iive 77; Mismatches 227;
                                                                                                                                                                                                                                                                                                             ORGANISM: Moloney murine leukemia virus
                                                                         Sequence 14, Application US/09309572
Patent No. 6440730
                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: env protein
US-09-309-572-14
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.0°
Matches 146; Conservative
                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-718-096-14
                                                                                                                                                                                                                                                                 SEQ ID NO 14
LENGTH: 665
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; Sequence 14, Application US/09718096

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 TAHTHMPR---NC----YNSATLCMHANTHYWTGK-----MINPSCPGGLGATVC-- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 PVLADOQPLSKPKPVKSP-----SVTKPPSGTPLSPTQLPPAGTENRLINLVDGAYQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 ALNLTSPDKTQECWLCLVAGPPYYEGVAVLGTYSNHTSAPANCSVASQHKLTLSEVTGQG 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 NKWCNPLVIRFTDAGRRVTSWTTGHYWGLRLYVSGQDPGLTFGIRLRYQNLGPRVPIGPN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QGQAREKQVKEAISQLTRGHSTPSPYKGLVLSKLH-ETLRTHTRLVSLFNTTLT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 -----HTSNLTCVKFSNTIDTTSSQCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNGS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPI---LPFVIRAGVLGRLGTG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 GGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTERW--GLLSQWMPW---- 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 LCIGAVPKTHQALC----NTTQTSSRGSYYLVA------PTGTWWACSTGLTPCISTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 IGSITT---STQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 RIHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTBINTTSVLVGPLVSNLEIT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --IDAPSYRSLSKGNSTF--
                     APPLICANT: Von Laer, Meike-Dorothee
TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----WTYFTHTSMSDGG---GI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.5%; Score 407.5; DB 4; 25.0%; Pred. No. 9.2e-33; ive 77; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SPYQEFLXRTRLPGN-
                                                      TITLE OF INVENTION: TAINCLAND TOTALE REPREBUCE: 35-195
CURRENT APPLICATION NUMBER: US/09/718,096
CURRENT FILING DATE: 2000-11-22
PRIOR PILING DATE: 1998-11-26
PRIOR PILING DATE: 1999-11-25
PRIOR PLING DATE: 1999-11-25
PRIOR PILING DATE: 1999-11-25
PRIOR PLING DATE: 1999-11-25
PRIOR PILING DATE: 1999-11-25
SEQUENCE: 1009-11-25
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 14
LENGTH: 665
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Moloney murine leukemia virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 PFALTAPPPCCCTTSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: env protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 25.0%
Matches 146; Conservative
GENERAL INFORMATION:
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US-09-315-127-11
                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                        919 PVLADQQPLSKPKPVKSP-----SVTKPPSGTPLSPTQLPPAGTENRLLNLVDGAYQ 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGSITT---STQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                             TAHTHMPR---NC----YNSATLCMHANTHYWTGK-----MINPSCPGGLGATVC-- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  799 CPGPHRPRESKSCGGPDSFYCAYWGCETTGRAYWKPSSSWDFITVNNNLTSDQAVQVCKD 858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QQQAREKQVKEAISQLTRGHSTPSPYKGLVLSKLH-ETLRTHTRLVSLFNTTLT 173
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APPLICANT: NATURE TECHNOLOGY, INC.
TITLE OF INVENTION: CHIMERIC VIRAL PACKAGING SIGNAL WITHOUT GAG GENE
TITLE OF INVENTION: SEQUENCES
FILE REFERENCE: 220:000130201
CURRENT APPLICATION NUMBER: US/09/554,572
CURRENT FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                  15.5%; Score 407.5; DB 4; Length 1312; 25.0%; Pred. No. 2.7e-32; tive 77; Mismatches 227; Indels 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448 VLPFLGPLAALILLLFGPCIFNLLVKFVSSRIEAVKLQMVLQ 490
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US-09-075-272-5
; Sequence 5, Application US/09075272
; Patent No. 6136598
; GENERAL INFORMATION:
    APPLICANT: WILLER, A. DUSTY
    APPLICANT: WOLGAMOT, GREG
; APPLICANT: WOLGAMOT, GREG
; APPLICANT: WOLGAMOT, GREG
; TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL
; TITLE OF INVENTION: PACKAGING CELL LINES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                    ) ORGANISM: Murine leukemia virus
US-09-554-572-26
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 146; Conserva
                                                                                                                                                                                  LENGTH: 1312
                                                                                                                                                               SEQ ID NO 26
                                                                                                                                                                                                      TYPE: PRT
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354 ----PYYEGIAQTRTYNITSDHSQCLWGENRKLTLTAVSGNGLCLGQVPQDKWHLCNQTQ 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 LRTHTRLVSLFNTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 TEQDLYNHVVPKPHNKRVPI---LPFVIRAGVLGR-LGTGIGSITTSTQFYYKLSQEING 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 DDSSFLDKFEHRVRWKREPITLTLAVLLGLGVAAAGVGTGTAALIQTPRYFEELRTAMDT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 KVKEIRDRIQCRAEELQNTERWGLLSQWM---PWVLPFL----GPLAALILLLLFGPCIF 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 LDTENRLVSLVOGAFLVLNRTNPNMTQSCWLC-----YASNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 VLVGPLVSNLEITHTSNLT-----CV-----KFSNTIDTTSSQCI--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The University of Tennessee, c/o Richard Cox
TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
FILE REFERENCE: 44137-5023, U. of Tennessee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                 ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 14.8%; Score 389.5; DB 3; Best Local Similarity 27.7%; Pred. No. 6.7e-31; Matches 106; Conservative 62; Mismatches 130;
                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,140
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INPORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 14538A-003710'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 NLLVKFVSSRIEAVKLQMVLQME 492
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                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/075,272
FILING DATE: 08-MAY-1998
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U.S.A.
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470

ug-09-319-156b-10.rai

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SGGGWPEGGENR-SPWFTTLISTIMGPLIVLLLILLFGFCILNRLVQFVKDRISVVQALV 630
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                                                                                                                                                         384 ALCNTTOSAGSGSYYLAAPAGTMWACSTGLTPCLSTTVLNLTTDYCVLVELWPRVIYHSP
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Patent No. 6448390

GENERAL INFORMATION:

APPLICANT: The University of Tennessee, c/o Richard Cox
TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
FILE REFERENCE: 44137-5023, U. of Tennessee
CURRENT APPLICATION NUMBER: US/09/315,127

CURRENT FILING DATE: 1999-05-20
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14.3%; Score 376.5; DB 4;
Best Local Similarity 28.4%; Pred. No. 1.4e-29;
Matches 103; Conservative 63; Mismatches 146;
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                                                                  340 AVVGTYTNHST--
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TYPE: PRT
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Sequence 12, Application US/09315127

Patent No. 6448390

FRENERAL INFORMATION:
APPLICANT: The University of Tennessee, c/o Richard Cox
TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
FILE REFERENCE: 44137-5023, U. of Tennessee
CURRENT APPLICATION NUMBER: US/09/315,127

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12
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                                                                                                                                                                                                                                 , Score 385; DB 4; Length 65; Pred. No. 1.9e-30; 60; Mismatches 154; Indels
CURRENT APPLICATION NUMBER: US/09/315,127
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN VEY: 2.0
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ORGANISM: Artificial Sequence
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US-09-315-127-11
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Matches 108; Conservative
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                                                                                                                      LENGTH: 654
TYPE: PRT
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Patent No. 6100034
GENERAL INFORMATION:
APPLICANT: Stoye, Jonathan P
APPLICANT: Weise, Robin A
TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope
FILE REFERENCE: 4238/75168
CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THTRLVSLFNTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFST-----
                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The University of Tennessee, c/o Richard Cox
APPLICANT: The University of Tennessee, c/o Richard Cox
TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
FILE REFERENCE: 44137-5023, U. of Tennessee
CURRENT APPLICATION NUMBER: US/09/315,127
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 645
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                                                                                                                        Sequence 9, Application US/09315127
Patent No. 6448390
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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VLQ 490
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US-09-111-085-2
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 GKGTCIGMVPPSHQHLCNHTBAFNRTSBSQYLVPGYDRWMACNTGLTPCVSTLVFNQTKD 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 MCFLSFLVPPMTIYTEQ---DLYNHVVPKPHNKRVPI---LPFVIRAGVLGRLGTGIGSI 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISTOFYYK----LSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGT 396
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                                                                                                                                                                                                                                                                                                                                                                           135 QLTRGHSTPSPY---KGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSAQNPTNCWMCLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   489 ITGPQQLEKGLSNLHRIVTEDLQALEKSVSNLEESLTSLSEVVLQNRRGLDLLFLKEGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLFLGEERCYYVNQSRIVTEKVKBIRDRIOCRAEELONTERWGLLSOWM---PWVLPFL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of Swine Retrovirus and Methods
                                                                                                                                                                                                                                                                                                                        71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:PERV-A OTHER INFORMATION: polypeptide sequence taken from GenBank Accession OTHER INFORMATION: No. 6261806 Y12238 for comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 376.5; DB 3; Length 660; Pred. No. 1.4e-29;
                                                                                                                                                                                                                                                                    Length 660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GPLAALILLLLFGPCIFNLLVKFVSSRIEAVKLOMVLOME 492
                                                                                                                                                                                                                                                               Query Match
14.3%; Score 376.5; DB 3;
Best Local Similarity 27.5%; Pred. No. 1.4e-29;
Matches 111; Conservative 68; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5. Application US/09376781
Patent No. 6261806
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Banerjee, Papia T.
APPLICANT: Banerjee, Clive
APPLICANT: Anderseon, Goran K.
TITLE OF INVENTION: Molecular Sequence of Sw.
FILE REPREMENT NO. 6261806
TITLE OF INVENTION: Use
FILE REPREMENT SETTION: 1999-08-18
CURRENT APPLICATION NUMBER: 60/097,015
BARLIER FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver: 2.0
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.3%;
27.5%;
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                                                                                                                                                             TYPE: PRT CRGANISM: Porcine retrovirus US-09-111-085-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 SGPPYYEGMARGGKFN-
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APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
                                               183 PINCWMCL----PLHF-----RPYISIPVPEQ----WNNFS----TEINTTSVLVGPLVSN 226
                                                                               362 HQ--HLCNHT-EAFN---QTSESQYLVPGYDRW--------WACNTGLTPCVS 400
                                                                                                                                                                                                                                            282 ----GSSESMCFLSFLVPPMTIYTEQ-----DLYNHVVPKPHNKRVPI---LPFVIRAG 328
                                                                                                                                                                                                                                                                                                                                     329 VLGRLGTGIGSITTSTQ----FYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRR 384
                                                                                                                                                                                                                                                                                                                                                                                                                                    385 ALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNT----ERWGL 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 GLDLLFLKEGGLCVALKEECCFYVDHSGAIRDSMNKLRERLEKRRREKETTQGWFEGWFN 575
242 IGPNTVLTGQRPPTQGPGPSSNITSGSDPTESSSTTKMGAKLFSLIQGAFQALNSTTPEA 301
                                                                                                                                             227 LEITHTSNLTCVKFSNTIDTTSSQCI----RWVTPPTRIVCLPSGIFFVCGTSAYHCLN 281
                                                                                                                                                                                                                                                                                 576 RSLWIATLLSALTGPLIVLLLLTVGPCIINKLIAFIRERISAVOI-MVLROO 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441 LSQWMPWVLPFL-GPLAALILLLLFGPCIFNLLVKFVSSRIEAVKLQMVLQME 492
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COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATURG SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/486,099

TILING DATE: 07-JUN-1995

TILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7872-031
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Patent No. 6013263
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CCRUZIL, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECHONICATION INFORMATION:
TELEPHONE: (212) 790-9904
TELEFACK: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bolognesi, Dani P. APPLICANT: Matthews, Thomas J. APPLICANT: Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66141 PENNIE
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                                                                               272 QEQRPSPNPSDYNTTSGSVPTEPNITIKTGAKLFSLIQGAFQALNSTTPEATSSCWLCLA 331
                                                                                                                                                192 LHFRPYISIPVPEQWNNFSTEINTTSVLVGPLVSNLEITHTSNLTCV-----KFSNTIDT 246
                                                                                                                                                                                               -----VTKEHRDQCTWGSQNKLTLTEVS 370
                                                                                                                                                                                                                                              247 TSSQCIRWYTPPTRIVCLPSGIF------FVGTSAYHCLN----GSSES 286
                                                                                                                                                                                                                                                                            371 GKGTCIGMVPPSHQHLCNHTEAFNRTSESQYLVPGYDRWWACNTGLTPCVSTLVFNQTKD 430
                                                                                                                                                                                                                                                                                                                                        287 MCFLSFLVPPMTIYTEQ---DLYNHVVPKPHNKRVPI---LPFVIRAGVLGRLGTGIGSI 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TTSTQFYYK----LSQEINGDMEOVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEBLQNTERWGLLSQWM---PWVLPFL- 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVALKEECCFYVDHSGAIRDSMSKLRERLERRRRERADOGW--FEGWFNRSPWMTTLLS 606
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                                                 135 QLTRGHSTPSPY---KGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSAQNPTNCWMCLP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Andersson, Goran K.

TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of Patent No. 6261806.

TITLE OF INVENTION: Use

TITLE OF INVENTION: Use

FILE REFERENCE: 61750-267

CURRENT PAPLICATION NUMBER: US/09/376,781

CURRENT FILING DATE: 1999-08-18

EARLIER APPLICATION NUMBER: 60/097,015

EARLIER APPLICATION NUMBER: 60/097,015

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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24.8%; Pred. No. 1e-28;
ive 82; Mismatches 187; Indels 132; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:PERV-C; OTHER INFORMATION: polypeptide sequence taken from GenBank Accession; OTHER INFORMATION: No. 6261806 AF038600 for comparison. US-09-376-781-6
    71;
  68; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GPLAALILLLEFGPCIFNLLVKFVSSRIEAVKLOMVLOME 492
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                                                                                                                                                                                               SGPPYYEGMARGGKFN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Banerjee, Papia T. APPLICANT: Patience, Clive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 132; Conservative
    Conservative
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Best Local Similarity
    Matches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-376-781-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549
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62 VVLQNRRGLDLLTAEQGGICLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPF 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 VVLQNRRGLDLLTAEQGGICLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPF 121
318 VPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAA 377
                                                                                   378 VVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTER 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 VVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTER 437
                        GENERAL INFORMATION:
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Maid, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IQLIPLFVGLGITTAVSTGAAGLGVSITQYTKLSHQLISDVQAISSTIQDLQDQVDSLAB
                                                                                                                                                                      438 WGLLSQWMPWVLPFLGPLAALILLLFGPCIFNLLVKFVSSRIEAVKLQMV 488
                                                                                                                                                                                            13.8%; Score 364; DB 3; Length 192; 39.8%; Pred. No. 3.9e-29; ive 44; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATARE: SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1155 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                   ; Sequence 107, Application US/08484223B
; Patent No. 6020459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERBNENCE/DOCKET NUMBER: 7872-1
TELECOMUNICATION INFORMATION:
TELEFHONE: (212) 790-9090
TELEFRAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 39.5%
....hes 68; Conservative
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-2238-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036-2711
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                               RESULT 23
US-08-484-223B-107
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                                                                                                                                               318 VPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAA 377
                                                                                                                                                                                                                                                           62 VVLQNRRGLDLLTAEQGGICLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNFF 121
                                                                                                                                                                                                                                    378 VVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTER 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wild, Carl T.
APPLICANT: Warney, Shawn O.
APPLICANT: Barney, Shawn O.
APPLICANT: Dennis M.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                438 WGLLSQWMPWVLPFLGPLAALILLLFGPCIFNLLVKFVSSRIEAVKLQMV 488
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                                                          13.8%; Score 364; DB 3; Length 192; 39.8%; Pred. No. 3.9e-29; Live 44; Mismatches 59; Indels
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39.8%; Pred. No. 3.9e-29;
.ive 44; Mismatches 59; Indels
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COUNTRY: USA
ZIP: 10036-271
ZIP: 10036-271
COMPUTER LEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMERS: 20-DEC-1994
FILING PATE: 20-DEC-1994
FILING PATE: 20-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 117, Application US/08360107A Patent No. 6017536 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 117:
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amino acid
                                                                                                       68; Conservative
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MOLECULE TYPE: protein
protein
                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
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US-08-360-107A-117
      US-08-486-099-107
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APPLICANT:
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RESULT 26
US-08-485-551A-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 VVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTER 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 VVLQNRRGLDLLTAEQGGICLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPF 121
                                                                                                                                                                                      Matthews, Thomas J.
Matthews, Thomas J.
Mild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
VENTION: METHODS AND COMPOSITIONS FOR INHIBITION
VENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
VENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IQLIPLFVGLGITTAVSTGAAGLGVSITQYTKLSHQLISDVQAISSTIQDLQDQVDSLAB 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 WGLLSQWMPWVLPFLGPLAALILLLFGPCIFNLLVKFVSSRIEAVKLQMV 488
438 WGLLSQWMPWVLPFLGPLAALILLLFGPCIFNLLVKFVSSRIEAVKLQMV 488
                       Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.8%; Score 364; DB 3;
39.8%; Pred. No. 3.9e-29;
tive 44; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-UUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7872-020
                                                                                                                                      Sequence 107, Application US/08919597 Patent No. 6054265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) /20 TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A. 742 REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
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APPLICANT: Lambert, Den
APPLICANT: Lamplois, St
APPLICANT: Lamplois, All
TITLE OF INVENTION: OF N
TITLE OF INVENTION: OF N
WIMBER OF SEQUENCES: 277
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
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Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bologn
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                                                                                                    RESULT 24
US-08-919-597-107
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378 VVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEBLQNTER 437
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Sequence 107, Application US/08475668A
Sequence 107, Application US/08475668A
Patent No. 666065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS: 221
CORRESPONDENCE ADDRESS: Remaine & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IQLIPLEVGLGITTAVSTGAAGLGVSITQYTKLSHQLISDVQAISSTIQDLQDQVDSLAB
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13.8%; Score 364; DB 3; Length 192;
Best Local Similarity 39.8%; Pred. No. 3.9e-29;
Matches 68; Conservative 44; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IDAD POW disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPAND SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REFERENCE/POCKET NUMBER: 30,742
REFERENCE/POCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 107, Application US/0848551A
Patent NO. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
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: New York
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318 VPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378 VVLONRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTER 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 WGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRIEAVKLQMV 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
13.8%; Score 364; DB 3; Length 192;
Best Local Similarity 39.8%; Pred. No. 3.9e-29;
Matches 68; Conservative 44; Mismatches 59; Indels
                                                                                                                                                                                           CURPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZI, LUMRA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
TELERRATION INFORMATION:
TELERRANIS (212) 790-9090
TELEBRAX: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOSITIONS FOR INHIBITION OF
                                          1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 107, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
                       ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds LLP
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APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Wild, Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: MEMBRANE FUSI
TITLE OF INVENTION: MEMBRANE FUSI
TITLE OF INVENTION: RESPIRATORY S
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 192 amino acids
TYPE: amino acid .
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                            ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
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ZIP: 10036-2711
                                                                                        New York
                                                               New York
                                                                                                                USA
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US-08-485-264A-107
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                                                                                                              COUNTRY:
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Matthews, Thomas J.
Mild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
VENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
VENTION: TRANSMISSION
VENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 VPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 VVLONRRALDLLTAKRGGTCLFLGEERCYYVNOSRIVTEKVKEIRDRIQCRAEELONTER 437
                                                     METHODS FOR INHIBITION OF MEMBRANE
FUSION-SSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TRANSMISSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.8%; Score 364; DB 3; Length 192; 39.8%; Pred. No. 3.9e-29; Live 44; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Proppy disk
COMPUTER: PREPARE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
TELEFAX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             B: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 107, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
                       Stephen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 192 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 39.8<sup>3</sup>
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                       Petteway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: C
TITLE OF INVENTION: F
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
                  APPLICANT: Petteway,
APPLICANT: Langlois,
TITLE OF INVENTION: ITILE OF INVENTION: ITILE OF INVENTION:
                                                                                                                                                                                                                                                 STATE: New York
                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                      USA
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US-08-471-913A-107
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STREET: 11
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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318 VPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: Matthews, Thomas J.
APPLICANT: With Carl T.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lambert, Dennis F.
APPLICANT: Lambert, Dennis F.
APPLICANT: Lambert, Dennis F.
ADPRESSEE: Pennis F.
Edmonds
ADPRESSEE: Pennis F.
Edmonds
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                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%; Score 364; DB 3; Length 192; 39.8%; Pred. No. 3.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                              7872-024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6479055
GENERAL INFORMATION:
                                     ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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NAME: Coruzzi, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION POR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 39.84
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                amino acid
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ZIP: 10036-2711
                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                       US-08-474-349A-107
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US-08-470-896-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 VPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 VVLQNRRGLDLITAEQGGICLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNFF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 3; Length 192;
3.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59; Indels
                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A FILING DATE: US-JUN-1995 CLASSIFICATION: 435
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; Pred. No. 3.9e
44; Mismatches
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TT: Matthews, Thomas J.
TT: Wild, Carl T.
TT: Lambert, Dennis M.
TT: Lambert, Dennis M.
TT: Langlois, Alphonse J.
TT: Langlois, Alphonse J.
TNVENTION: COMPOSITIONS FOR IN
                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REBERENCE/DOCKET NUMBER: 7872-021
TELEPHONE: (212) 790-9090
TELEPAX: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
TELEFAX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Pennie & Edmonds
1155 Avenue of the Americas
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Patent No. 6333395
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.8%;
39.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 39.8<sup>3</sup>
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Matthews, The APPLICANT: Walthews, The APPLICANT: Barney, Shaw APPLICANT: Lambert, Dent APPLICANT: Lambert, Dent APPLICANT: Lambert, Dent APPLICANT: Lambert, Dent TITLE OF INVENTION: COMMITTEE OF INVENTION: FUSING OF INVENTION: VIRK NUMBER OF SEQUENCES: 517 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER READABLE FORM:
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: New York
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APPLICANT: Bologn
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US-08-474-349A-107
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318 VPILPFVIRAGVIGRIGGIGSITTSTQFYYKLSOBINGDMEQVTDSLVTLODOLNSLAA 377
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13.8%; Score 364; DB 4; Length 192;
Best Local Similarity 39.8%; Pred. No. 3.9e-29;
Matches 68; Conservative 44; Mismatches 59; Indels
| TELEPHONE: (212) 790-9090
| TELEFAX: (212) 869-9741/8864
| TELEX: 66141 PENNIE
| INFORMATION FOR SEQ ID NO: 107:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 192 amino acids
| TYPE: amino acid
| TYPE: amino acid
| STRANDEDNESS:
| TOPOLOGY: unknown
| MOLECULE TYPE: protein
| US-08-470-896-107
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Search completed: January 22, 2005, 22:12:41 Job time : 48 secs

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January 22, 2005, 22:07:21; Search time 106 Seconds (without alignments) 1680.336 Million cell updates/sec
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16: /cgn2_6/ptodata/2/pubpaa/USOO_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USOO_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USOO_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 106, App	Sequence 106, App	Sequence 2, Appli	Sequence 20, Appl	Sequence 2, Appli	Sequence 135, App	Sequence 4, Appli	Sequence 2, Appli	Sequence 21, Appl	Sequence 20, Appl	Sequence 37656, A	Sequence 473, App	Sequence 4, Appli
SUMMARIES	US-08-979-847-106	US-10-114-104-106	US-10-416-642-2	US-10-637-565-20	US-09-902-535-2	US-10-114-893-135	US-10-016-249-4	US-10-133-036-2	US-10-133-036-21	US-10-133-036-20	US-09-864-761-37656	US-10-363-616-473	US-10-133-036-4
DB	8	14	15	15	σ	13	14	15	15	15	0	15	15
% Query Match Length DB ID	493	493	542	503	538	538	538	538	538	538	263	531	120
% Query Match	99.9	99.9	92.9	91.8	88.0	88.0	88.0	87.9	86.8	84.9	46.9	42.6	22.4
Score	2632	2632	2447	2419	2319	2319	2319	2314	2285	2237	1235.5	1122	591
Result No.	1	7	3	4	S	Q	7	80	თ	10	11	12	13

Sequence 109, App Sequence 109, App	4,	Seguence 4, Appli	Sequence 4, Appli	7	Sequence 81, Appl	e 87,	81,	297	Seguence 1749, Ap	귺	ω	4	φ̈́	ທີ	Sequence 7, Appli	9	۲,	4	4	4	36	38	'n	e ø	ដ	76	78	Seguence 43, Appl	Seguence 4, Appli	Seguence 2, Appli
ם	3		14 US-10-283-903-4	13 US-10-001-835-168	8 US-08-979-847-81	14 US-10-430-442-87	US-10-114-104	10 US-09-764-891-2970	15 US-10-276-774-1749	9 US-09-954-983-11	9 US-09-954-983-8	9 US-09-954-983-4	9 US-09-954-983-6	9 US-09-954-983-5	9 US-09-954-983-7	16 US-10-441-949-32	16 US-10-441-949-34	US-10-441		16 US-10-441-949-45	16 US-10-441-949-36	US-1	9 US-09-851-859A-5	16 US-10-441-949-8	16 US-10-441-949-10	16 US-10-441-949-16	16 US-10-441-949-18			14 US-10-029-656-2
162 162	576	216	576	469	433	433	433	253	618	9/9	675	672	675	672	675	638	638	638	638	638	678	678	099	099	099	099	099	661	653	653
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516 516	514.5	514.5	514.5	480.5	452	452	452	423	421	393	392	391	389	386	386	378	378	378	378	378	378	378	376.5	376.5	376.5	376.5	376.5	376.5	374.5	372.5
14	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Datent Nelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
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                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-2787
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,104
FILING DATE: 03-Apr-2002
CLASSIPICATION: <Unknown>
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TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 106:
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
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               ADDRESSEE: OLIFF & BER
STREET: P.O. BOX 19928
                                                                                                                         ZIP: 22320
COMPUTER READABLE FORM:
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                                                    CITY: ALEXANDRIA STATE: VA COUNTRY: USA
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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                                                                                                                                                                                                                                                                                              99.9%; Score 2632; DB 8; Length 493;
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                                                                                                                                                                                                                                                                                                                  5.4e-240;
                                                                                                                                                                                                                                                                                                           100.0%; Pred. ...
               REFERENCE/DOCKET NUMBER: WPB 39046A TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-10-114-104-106
; Sequence 106, Application US/10114104
; Publication No. US20030198647A1
; GENERAL INFORMATION:
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BEDIN, FREDERIC
PARANHOS-BACCALA, C
KOMURIAN-PRADEL, FI
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GARSON, JEREMY
TUKE, PHILIP
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30,024
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                                                                                                                                             LENGTH: 493 amino acida
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                        Matches 493; Conservative
                                                                                                                                                                                         single
REGISTRATION NUMBER:
                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
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Best Local Similarity
                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF
                                                                                                                                                                                                                                                    US-08-979-847-106
                                                                                                                                                                                                               TOPOLOGY:
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SEQ ID NO 20
LENGTH: 503
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US-09-902-535-2
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; OTHER INFORMATION: Incyte ID No. US20040043452A1 7477736CD1
US-10-416-642-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Indels
                                                                                                                    APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: ARVIZU, Chandra
TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
FILE REFERENCE: PP-0842 PCT
CURRENT APPLICATION NUMBER: US/10/416,642
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2447; DB 15;
Pred. No. 2.1e-222;
8; Mismatches 26;
                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 08/10/410
PRIOR APPLICATION NUMBER: 60/249,407
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 2
TENNAM:
                                                                          ; Sequence 2, Application US/10416642; Publication No. US20040043452A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.9%;
Best Local Similarity 93.1%;
Matches 459; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
481
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RESULT 4 US-10-637-565-20 ; Sequence 20, Application US/10637565

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APPLICANT: PERRON, Herve
APPLICANT: KOMURIAN-PRADEL, Florence
TITLE OF INVENTION: THE LTR REGION OF MSRV-1 AND THE PROTEINS IT ENCODES, AND PROBES
TITLE OF INVENTION: METHODS FOR DETECTING MSRV-1 RETROVIRUS
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Patent No. US20020102530A1;
GENERAL INFORMATION:
APPLICANT: Keith, Jr., James C.
APPLICANT: McCoy, John M.
TITLE OF INVENTION: Methods and compositions for diagnosing
TITLE OF INVENTION: and treating preeclampsia and gestational trophoblast;
TITLE OF INVENTION: disorders;
FILE REFERENCE: GIN-6006B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 RTRLPGNIDAPSYRSLSKGNSTFTAHTHMPRNCYNSATLCMHANTHYWTGKMINPSCPGG
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                                                                                                                              THIS REFERENCE: 110257
CURRENT APPLICATION NUMBER: US/10/637,565
CURRENT FILING DATE: 2003-08-11
PRIOR PEDILCATION NUMBER: US/09/890,340
PRIOR APPLICATION NUMBER: DCT/IBOO/00159
PRIOR FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: PCT/IBOO/00159
PRIOR PLILING DATE: 2000-02-15
PRIOR PLILING DATE: 1999-02-15
PRIOR PLILING DATE: 1999-02-15
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
APPLICANT: PARANHOS-BACCALA, Glaucia
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US-10-637-565-20
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US-10-016-249-4
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APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Yenneth
APPLICANT: Lavalile, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Kelleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
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                                                                                                                                                                                                                                                                        Query Match

88.0%; Score 2319; DB 9;
Best Local Similarity 88.6%; Pred. No. 2.7e-210;
Matches 436; Conservative 18; Mismatches 38;
CURRENT APPLICATION NUMBER: US/09/902,535
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/216,657
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 538
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                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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US-10-114-893-135
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Sequence 4, Application US/10016249
; Sequence 4, Application US/10016249
; Publication No. US20030100053A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Lafallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Treacy, Maurice
; APPLICANT: Heacy, Maurice
; APPLICANT: Mi, Sha
; APPLICANT: Mi, Sha
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; TITLE OF INVENTION: SECRETED PROTEINS
; TITLE REPREBUCE: 60068.AJ172A
; CURRENT FILING DATE: 2001-10-30
; PRIOR PLICATION NUMBER: US/10/016,249
; CURRENT FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 62
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CURRENT FILING DATE: 2002-04-02
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 135
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; ORGANISM: Homo sapiens
US-10-114-893-135
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  MALPYHTFLFTVLLPPFALTAPPPCCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSKGNS
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Sequence 21, Application US/10133036

Publication No. US2004054133A1

GENERAL INFORMATION:

APPLICANT: Contrad, Bernard

TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen

PILE REPERENCE: 23135-507

CURRENT APPLICATION NUMBER: US/10/133,036

CURRENT FILING DATE: 2002-04-26

PRIOR APPLICATION NUMBER: PCT/EP00/10659

PRIOR PILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PatentIn Ver. 2.1

SOFTWARE: PATENTING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PATENTING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PATENTING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PATENTING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PATENTING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PATENTING DATE: 2000-10-30
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481 EAVKLQMEPKMQ 492
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US-10-133-036-21
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                                                                                                                                                   88.0%; Score 2319; DB 14;
88.6%; Pred. No. 2.7e-210;
iive 18; Mismatches 38;
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APPLICANT: Conzad, Bernard
TITLE OF INVENTION: Multiple Sclerosis-Related Sup;
FILE REFERENCE: 23135-507
CURRENT APPLICATION NUMBER: US/10/133,036
CURRENT FILING DATE: 2002-04-26
FRIOR APPLICATION NUMBER: PCT/EP00/10659
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human endogenous retrovirus
US-10-133-036-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10133036 Publication No. US20040054133A1 GENERAL INFORMATION:
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SOFTWARE: Patentin Ver.
SEQ ID NO 4
LENGTH: 538
                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                            Similarity
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US-10-133-036-2
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Best Local S
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420 480

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APPLICANT: Rank, SHARTON G.
APPLICANT: Rank, SHARTON G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
ATITLE OF INVESTION: GREW EXPRESSION AAALYSIS BY MICROARRAY
FILE REFERENCE: Account G. 2.2
FILE REFERENCE: Account G. 2.2
CORREMY PALLING DAVE: 2000 -02-22
PRIOR FILING DAVE: 2000 -02-22
PRIOR FILING DAVE: 2000 -02-23
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PRIOR FILING DAVE: 2001 -02-23
PRIOR FILING DAVE: 2001 -02-23
PRIOR PLICATION WINDER: PCT/USC1/00663
PRIOR FILING DAVE: 2001 -02-23
PRIOR PLICAMING DAVE: 2001 -02-23
PRIOR FILING DAVE: 2001 -02-23
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PRIOR PLICAMING DAVE: 2000 -02-23
PRIOR PL
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                                                                    361 VTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKE
                                                                                                                                 421 IRDRIQCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRI
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Patent No. US20020048763A1
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ORGANISM: Homo sapiens
PERJUNE:
OTHER INFORMATION: MAP TO AC002346.1
                                                                                                                                                                                                                          481 EAVKLOMVLOME 492
                                                                                                                                                                                                                                                                   481 EAVKLOMEPKMQ 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONPINCWMCLPLHFRPYISIPVPEQWNNFSTEINTISVLVGPLVSNLEITHTSNLTCVKF 240
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                                                                                                                                                                                                                               IRDRIQCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRI 480
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                                                                                                                                                                                                                                                                                          VTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKE 420
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                           TEQDLYNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQ
                                                                                                                 SNTIDITSSOCIRWYTPPTRIVCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIY
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APPLICANT: Mach, Bernard
TITLE OF INVESTION: Maltiple Sclerosis-Related Superantigen
FILER REPERENCE: 23135-507
CURRENT APPLICATION NUMBER: US/10/133,036
CURRENT PILICA DATE: 2002-04-26
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 20
LENGTH: 538
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85.6%; Pred. No. 1.6e-202;
iive 26; Mismatches 45; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 20, Application US/10133036; Publication No. US20040054133A1; GENERAL INFORMATION:
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Best Local Similarity 85.6%
Matches 421; Conservative
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ORGANISM: Retrovirus
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10-133-036-20
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VIRAL MATERIAL AND NUCLEOTIDE FRACMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
THERAPEUTIC PURPOSES
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                             197 YISIPVPEOWNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKFSNTIDTTSSOCIRWVT 256
                                                                                                          257 PPTRIVCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNK 316
                                                                                                                                      -----VPPMTIYTEQDLYNHVVPKPHNK 234
                                                                                                                                                                                           RVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLA 376
                                                                                                                                                                                                                                                                            377 AVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTF 436
                                                                                                                                                                                                                                                                                                                295 AVVLONRRALDILITAKRGGTCLFLGEECCYYVNQSRIVTEKVKBIRDRIQCRAEELQNTE 354
                                                                                                                                                                                                                               235 RVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLA 294
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                                                                                                                                                                                                                                                                                                                                                           437 RWGLLSQWMPWVLPFLGPLABLILLLFGPCIFNLLVKFVSSRIEAVKLQWVLQMEP 493
                                                                                                                                                                                                                                                                                                                                                                                355 HWGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRIEAVKLQMVLQMEP 411
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Publication No. US20040054133A1

GENERAL INFORMATION:
APPLICANT: Conrad, Bernard
TITLE OF INVENTION: Multiple Sclerosis-Related Sup;
FILE REFERENCE: 23135-507
CURRENT FILING DATE: 2002-04-26
PRIOR FILING DATE: 2002-04-26
PRIOR FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 1.4e-47;
3; Mismatches 13;
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FLORENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 109, Application US/08979847
; Publication No. US20030039664A1
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KOMURIAN-PRADEL,
JOLIVET-REYNAUD,
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GARSON, JEREMY
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BESEME, FREDERIC
BEDIN, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.7%;
Matches 104; Conservative
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TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BFGKNKKQRSNLQATSLISCAT-----VLBTRSPRSRCWQVQCLVKAILPFQDDTLLTHP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ANTHYWTGKMINPSCPGGLGATVCWTYFTHTSMSDGGGIQGQAREKQVKEAISQL 136
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N: EXPRESSED IN PLACENTA, SIGNAL = 20

N: EXPRESSED IN HBL100, SIGNAL = 6

N: EXPRESSED IN HBL100, SIGNAL = 5.4

N: EXPRESSED IN BT474, SIGNAL = 5.9

N: EXPRESSED IN FETAL LIVER, SIGNAL = 6.7

N: EXPRESSED IN ADULT LIVER, SIGNAL = 6.7

N: EXPRESSED IN BRAIN, SIGNAL = 6.2

N: EXPRESSED IN HOUT, SIGNAL = 6.3

N: EXPRESSED IN HONG, SIGNAL = 3.9

N: EXPRESSED IN HELA. SIGNAL = 7.2

NN: EXPRESSED IN HELA. SIGNAL = 7.2

NN: EXPRESSED IN HELA. SIGNAL = 7.2

NN: EXPRESSED IN HELA. SIGNAL = 7.2

NN: EXPRESSED IN HELA. SIGNAL = 7.2

NN: EXPRESSED IN HELA. SIGNAL = 7.2
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                                                                                                                                                                                                                                                                                                                                        19; Indels
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
                                                                                                                                                                                                                                                                                                 DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1122; DB 15;
Pred. No. 6.2e-97;
6; Mismatches 29;
                                                                                                                                                                                                                                                                                               Score 1235.5; DB
Pred. No. 4e-108;
8; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 VTLQDQLNSLAAVVLQNRRALDLL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTLQDQLNSLAAVVLQNRRALDLL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 473, Application US/10363616 Publication No. US20040044181A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/654,935
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 473
                                                                                                                                                                                                                                                                                               46.9%;
89.4%;
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ilarity 51.6%;
Conservative
                                                                                                                                                                                                                                                                                                                     Best Local Similarity 89.4
Matches 236; Conservative
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-363-616-473
                       OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E OTHER INFORMATION: E
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                       US-09-864-761-37656
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US-10-363-616-473
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Best Local S
Matches 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LSOWMPWTLPFLGPLAAIIFLLFGPCIFNFLVKFVSSRIBAVKLQIVLOMEP 113
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APPLICANT: ATENIA B. KARLAND
APPLICANT: Gazelle S. Rastegar
APPLICANT: Gazelle S. Rastegar
APPLICANT: Gazelle S. Rastegar
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Pia M. Challita-Eid
APPLICANT: MAY FARIS
TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
FILE REFERENCE: 129 215512
CURRENT APPLICATION NUMBER: 05/09/793,451
CURRENT FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 752
SOFTWARE: FASTESEQ FOR WINDOWS VERSION 4.0
LENGTH: 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.6%; Pred. No. 2.7e-40;
Matches 99; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLING DATE: 03-Apr-2002
CLASSIFICATION: <unversion*
CLASSIFICATION: <unversion*
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ilarity 25.5%; Pred. No. 2.4e-39;
Conservative 63; Mismatches 123;
                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-5787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 162 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09793451
Publication No. US20030157597A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: homo sapiens
US-09-793-451-4
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Best Local Similarity
Matches 142; Conserv
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440
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                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
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ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
AUDRESS:
CLIFF & BERRIDGE, PLC
SET: P.O. BOX 19928
ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-114-109, Application US/10114104
; Sequence 109, Application US/10114104
; Publication No. US20030198647A1
; GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
RESEME, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-836-278/
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
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TUKE, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 162 amino acids
amino acid
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                                                                                                                                                                                                                                                                    ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                         ADDRESSEE:
STREET: P.
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| ::| | | ATAVPAVQTDWATSPISLHLRTSFNSPHLYPPEELIYFLDRSSKTSPDISHQQAAALLR 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 GTEELPVPLMTPTQQKRVIPLIPLMVGLGLSASTVALGTGIAGISTSVMTFRSLSNDFSA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 HSTPSPYKGLVLSKLHETLR-THTRLVSLFNTTLTRLHEVSAQNPT---NCWMCLPLHFR 195
                                                                                                                                                                                                                                                                                                                                                                                         186 PTTNINETIGAFQLHITDKPSINTDKLKN---ISSNYCLGRHLPCISLHPWLSSPCSSDS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 PPRPSSCLLIPSPENNSERLLVDTRRFLIHHENRTFPSTQLPHQSPLQPLTAAALAGSLG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 -WV--TP---PTRI-----VCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIY- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 -TEQDLYNHVVPKPHNKRVPILPFVIRAGVLG---RLGTGIGSITTSTQFYYKLSQEING 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 DMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 KVKEIRDRIQCRAEELQNTER--WGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 HPLPLP-----SYLHHTINLTHSLL------AASNPSLVNNCWLCISLSSS
Query Match 19.5%; Score 514.5; DB 14; Length 576; Best Local Similarity 25.5%; Pred. No. 2.4e-39; Matches 142; Conservative 63; Mismatches 123; Indels 229; Gaps
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US-10-283-903-4

i Sequence 4, Application US/10283903

i Sequence 4, Application No. USZ020319766A1

i GENERAL INFORMATION:

i APPLICANT: Arthur B. Raitano

APPLICANT: Daniel E.H. Afar

APPLICANT: Gazelle S. Rastegar

APPLICANT: Rene S. Hubert

APPLICANT: Pia M. Challita-Eid

APPLICANT: Pia M. Challita-Eid

APPLICANT: Pay Jackbovits

TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS

TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS

TITLE OF INVENTION: UNMBER: US/10/283,903

CURRENT APPLICATION NUMBER: US/10/283,903

PRIOR APPLICATION NUMBER: US/09/793,451

PRIOR FILING DATE: 2000-02-26

PRIOR FILING DATE: 2000-02-26

PRIOR FILING DATE: 2000-02-26

PRIOR FILING DATE: 2000-02-26

PRIOR FILING DATE: 2000-02-26

PRIOR FILING DATE: 2000-07-13

NUMBER OF SEQ ID NOS: 752

SEQ ID NO 4
                                                                                                                                                                                             196 PYISIP-VPEQW-----
                                                                                                                                                                                                                                                                                          207 ---NNFSTEINTTSVLVGPLVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: :||:|:
542 FIQNRIQAITNHSIRQM 558
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                                                                                                                                                                                                                           363 GTEELPVPLMTPTQQKRVIPLIPLMVGLGLSASTVALGTGIAGISTSVMTFRSLSNDFSA 422
  HSTPSPYKGLVLSKLHETLR-THTRLVSLFNTTLTRLHEVSAQNPT---NCWMCLPLHFR 195
                                                                                                                                           66 AYTAVPAVQTDWATSPISLHLRTSFNSPHLYPPEBLIYFLDRSSKTSPDISHQQAAALLR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                      243 PPRPSSCLLIPSPENNSERLLVDTRRFLIHHENRTFPSTQLPHQSPLQPLTAAALAGSLG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 -WV--TP---PTRI-----VCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIY- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 VWVQDTPFSTPSHLFTLHLQFCLAQGLFFLCGSSTYMCLPANWTGTCTLVFLTPKIQFAN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TEQDLYNHVVPKPHNKRVPILPFVIRAGVLG---RLGTGIGSITTSTQFYYKLSQEING 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 DMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 KVKEIRDRIQCRAEELQNTER--WGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVK 474
                                186 PTTNINETIGAFQLHİTDKPSINTDKLKN---ISSNYCLGRHLPCISLHPWLSSPCSSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Arthur B. Raitano
APPLICANT: Daniel E.H. Afar
APPLICANT: Gazelle S. Rastegar
APPLICANT: Gazelle S. Rastegar
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Fene S. Hubert
APPLICANT: Pia M. Challita-Eid
APPLICANT: Pia M. Challita-Eid
APPLICANT: Pia M. Challita-Eid
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APPLICANT: Pia M. Challita-Eid
APPLICANT: NAV Jakobovits
TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129 -218012
CURRENT APPLICATION NUMBER: US/10/283,722
CURRENT FILING DATE: 2000-02-26
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/184,558
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-07-13
                                                                                                                                                                                           207 ---NNFSTEINTTSVLVGPLVS------
                                                                                                                                                                                                                                                                                            ------NLEITHTSNLTCVKFSNTIDTTSSQCIR-
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SOFTWARE: FastSEQ for Windows Version 4.0
                                     26 HPLPLP-----SYLHHTINLTHSLL---
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542 FIQNRIQAITNHSIRQM 558
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ORGANISM: homo sapiens
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LENGTH: 576
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VIRAL MATERIAL AND NUCLEOTIDE FRACMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACTI
THERAPEUTIC PURPOSES
                                                                                                                                              53 ISRQRPTGIPLGNLSPSRCSFTLHLRSPTTHITETIGAFQLHITDKPSINTDKLKNISSN 112
                                                                                                                                                                                               213
                                                                                                                                                                                                                                                                                                                167 HENRTS-----PSTQLPHQSPLOPLTAASLAGSLGI------WVQDTPFSTPHLFTL 212
                                                                                                                                                                                                                                                                                                                                                                                           213 HLOPCLTOGLFFLCGSSTYMCLPANWTGTCTLVFLTPKIOFANGTEELPVPLMTPTROKR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                     317 RVPILLPFVIRAGVLG----RLCTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---RLHEVSAQ 181
                                                                                                                                                                                                                                  113 -----YCLGRHLPSISLHPWLPSPCSSDSPPRPSSRLLIPSPKNNSERLLVDTQRFLIH 166
                                                                                                                                                                                                                                                                                                                                                        263 ----CLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIY--TEQDLYNHVVPKPHNK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 SLAAVVIQNRRALDILITAKRGGICLFIGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQ 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     491
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                                                                                                                                                                                                                                                                              214 --NTTSVLVGPLVSNLEITHTS---NLTCVKFSNTIDTTSSQCIRWV-----TPPTRIV
                                                                                                                                                                                            182 NPTNCWMCLPLHF---------RPYISIPVPEQWNNFSTEI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 NTER--WGLLSQWMPWVLPFLGPLAALILLLFGPCIFNLLVKFVSSRIBAVKLQMVLQM
                                                                           Gaps
                                                                           85;
                                   Length 469;
                                                                           Indels
                                                                                                                 136 LTRGHSTPSPYKGLVLSKLHETLR----TH-TRLVSLFNTTLT-
                                   DB 13;
                               18.2%; Score 480.5; DB 13;
31.4%; Pred. No. 3e-36;
tive 62; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.30
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NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BESEME, FREDERIC
APPLICANT: BEDIN, FREDERIC
APPLICANT: PARANGOS-BACCALA, GLAUCIA
APPLICANT: KOMURIAN-PRADEL, FLORENCE
APPLICANT: MANDRAND, COLETTE
APPLICANT: MANDRAND, BERNARD
APPLICANT: GARSON, JEREWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 81, Application US/08979847
Publication No. US20030039664A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERRON, HERVE
                                     Query Match 18,23
Best Local Similarity 31.43
Matches 132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TUKE, PHII
TITLE OF INVENTION: I
TITLE OF INVENTION: I
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OPERATING SYSTEM:
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US-10-001-835-168
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APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
FILE REFERENCE: DEX-0277
CURRENT APPLICATION NUMBER: US/10/001,835
CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-20
                                                                                                                                          16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 WWVQDTPFSTPSHLFTLHLQFCLAQGLFFLCGSSTYMCLPANWTGTCTLVFLTPRIQFAN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TEQDLYNHVVPKPHNKRVPILPFVIRAGVLG---RLGTGIGSITTSTQFYYKLSQEING 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 DMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVKEIRDRIQCRAEELQNTER--WGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVK 474
                                                                                                                                                                                                                                                                                                   66 AYTAVPAVQTDWATSPISLHLRTSFNSPHLYPPRELIYFLDRSSKTSPDISHQQAALLR 125
                                                                                                                                                                                                                                                                                                                                                                                   126 TYLKNLSPYİNSTPPIFGPLTTQTTIPVAAPLCISWQRPTGIPLGNLSPSRCSFTLHLRS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 PPRPSSCLLIPSPENNSERLLVDTRRFLIHHENRTFPSTQLPHQSPLQPLTAAALAGSLG 302
                                                                                                                                                                                140 HSTPSPYKGLVLSKLHETLR-THTRLVSLFNTTLTRLHEVSAQNPT---NCWMCLPLHFR 195
                                                                                                                                                                                                                        186 PITNINETIGAFQLHİTDKPSINTDKLKN---ISSNYCLGRHLPCISLHPWLSSPCSSDS
                                                                                                                                          Gaps
                                                                                                Query Match
19.5%; Score 514.5; DB 14; Length 576;
Best Local Similarity 25.5%; Pred. No. 2.4e-39;
Matches 142; Conservative 63; Mismatches 123; Indels 229;
                                                                                                                                                                                                                                                                                                                                                                                                                             ------NLEITHTSNLTCVKFSNTIDTTSSQCIR----
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                                                                                                                                                                                                                                                                                                                                               ---NNFSTEINTTSVLVGPLVS---
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FIQNRIQAITNHSIRQM 558
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 168
LENGTH: 469
TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Salceda, Susana APPLICANT: Macina, Roberto
                    TYPE: PRT ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 19
US-10-001-835-168
  LENGTH: 576
                                                              US-10-283-903-4
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL.
THERAPEUTIC PURPOSES
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                                                                                                                                                                                                                                                                                                                               334 GTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 GGTCLFLGEERCYYVNQSRIVTEKVKEIRDRI----QCRAEELQNTERWGLLSQWMPWVL 449
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                     Length 433;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                              17.2%; Score 452; DB 14;
54.3%; Pred. No. 1.3e-33;
iive 27; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14-104-81

19:10-114-104-81

19:20-114-104-81

19:ENERAL 10:20030198647A1

19:ENERAL INFORMATION:

10:ENERAL INFORMATION:

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APPLICATION NUMBER: US/10/114,104
FILING DATE: 03-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BERRIDGE, PLC
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BERRIDGE, WILLIAM P. REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 81:
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOMURIAN-PRADEL,
JOLIVET-REYNAUD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERI
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                    Query Match
Best Local Similarity 54.39
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: VA
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                                                                                                                                 US-10-430-442-87
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 GGTCLFLGEERCYYVNQSRIVTEKVKEIRDRI----QCRAEELQNTERWGLLSQWMPWVL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 GTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 GGLCTFLGEECCFYTNQSGIVRDATWHLQERASDIRQCLSNSYTN-----LWSWATWLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8; Length 433;
1.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFLGPMAAILLLITFGPCIFKLLVKFVSSRIEAIKLQMVLQMEP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFLGPLAALILLLFGPCIFNLLVKFVSSRIEAVKLQMVLQMEP 493
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38588
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/691,563
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/430,442 FILING DATE: 07-May-2003 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                17.2%; Score 452; 54.3%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Frederic BESEME
Frederic BEDIN
Glaucia PARANHOS-BACCALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Florence KOMURIAN-PRADEL
Colette JOLIVET
Bernard MANDRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 87, Application US/10430442
Publication No. US20030186391A1
GENERAL INFORMATION:
APPLICANT: Herve PERRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
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   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                             not relevant
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                                                                                                                                                                   LENGTH: 433 amino acids TYPE: amino acid
                                                         TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 54.3
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 21
US-10-430-442-87
                                                                                                                                                                                                                                                                                                                                   US-08-979-847-81
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us-09-319-156b-10.rapb

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                                                                                                                                                                                                                                                   66 GGLCTFLGEECCFYTNQSGIVRDATWHLQBRASDIRQCLSNSYTN-----LWSWATWLL 119
                                                                                                                                                   334 GTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKR 393
                                                                                                                                                                                                                            GGTCLFLGEERCYYVNQSRIVTEKVKEIRDRI----QCRAEELQNTERWGLLSQMMPWVL 449
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 SAYHCLNGSSESMCFLSFLVP-----PMTIYTEQDLYNHVVPKPHNKR-VPILP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (162)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-2970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 FVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQN 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRI-QCRAEELQNTERWGLL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2970, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 10231
; SEQ ID NO 2970
; SEQ ID NO 2970
; LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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                                                                            Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 WKWXSWVLPLTGPLXSLLLLLLFGPCLLNLITQFVSSRLQAIKLQ 236
                                                                        Query Match 17.2%; Score 452; DB 14; Length 43
Best Local Similarity 54.3%; Pred. No. 1.3e-33;
Matches 89; Conservative 27; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                        PFLGPMAAILLLTFGPCIFKLLVKFVSSRIEAIKLOMVLOMEP 163
                                                                                                                                                                                                                                                                                                     PFLGPLAALILLLFGPCIFNLLVKFVSSRIBAVKLOMVLOMEP 493
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 81:
US-10-114-104-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 39.19
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 23
US-09-764-891-2970
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RESULT 24 US-10-276-774-1749

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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 1749
LENGTH: 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 TOXFTA---LPADLLTWTQSNVSLHISYLAIPFLADSFLKPVLXPGNSAKHLSFKLSSLS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 MVSGRAV---ALLHLIASGLTSIQTNTASSKPPIWGY-----LSTQTSFISPPLCL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 SRTY----PNPAHATMVGQVPQSLCGLIFTLRTPCRPSILHPNYKIISTSAWQKVLCFSG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 SPTIHTSLHLTTGSSFLSFHPIPGFPAANSALYVSSLKGPPGKNVTIPSPVTGTXQPPHR 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CIRWVTPPTRI 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 HNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 SLAAVVLONRRALDLLTAKRGGTCLFLGEERCYYVNOSRIVTEKVKEIRDRIOCRAEEL- 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 HKFLF-LLLPSLLMGYSESPPP--ITDSWAPPISLTHHVLSQSQSP--LSSNCWICLSTH 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 HTFLFTVLLPPFAL---TAPPPCCCTTSSSPY----QEFLXRTRLPGNIDAPSYRSLSKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 NSTFTAHTHMPRN--CYNSATLCMHAN---THYWTGKMINPSCPGGLGATVCWTYFTHTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 MSDGGGIQGQAREKQVKEAISQL-TRGHSTPSPYKGLVLSKLHETLRTHTRLVSLFNTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----CLPLHFRPYISIPVPEQWNN---FS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 16.0%; Score 421; DB 15; Length 618;
Best Local Similarity 26.5%; Pred. No. 1.9e-30;
Matches 157; Conservative 77; Mismatches 214; Indels 144; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             529 HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLFLLIMIGPCIFNLVSRFISQRL 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1). ... (618)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-276-774-1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 -TSNLTCVKFS-----NTIDTTSSQ-----
Sequence 1749, Application US/10276774
Publication No. US20040053245A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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US-09-954-983-11
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LTQ 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 TAHTHMPR---NC----YNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFT-HT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PANCSAASQHKLTLSEV----TGRGLCIGTVPKTHQALCNTTLKTGKGSYYLVAPAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 IFFVCGTSAYHCLNGS----SESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPI--- 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPFVIRAGVLGRLGTGIGSITT---STQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVLQNRRALDLITAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTER 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::: :: NITTINQAVQVCKDNKWCNPLAIRFTNAGRQVTSWTTGHSWGLRLYVTGKDPGLTFGIRLK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 YONLGPRVPIGPNPVLADQLSFPLPNPQPKPAKSPPASNSTPTLISPSPTPTQPPPAGTG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRLVSLFNTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 DRLLINLVQGAYQALNLTNPDKTQECWLCLVSGPPYYEGVAV-----LGTYSNHTS---A 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 W--GLLSQWMPW----VLPFLGPLAALILLLLFGPCIFNLLVKFVSSRIEAVKLQMVLQ 490
                                                                                                                                                                                                                                                                                                                                                                                                        ---LPSG
                                                                                                                                                                                                                                                                                                                                                                                    16 PFALTAPPPCCCTTS-----SSPYQEFLXRTRLPGN---IDAPSYRSLSKGNSTF
                                                                                                                                                                                                                                                                                                                                                      81; Mismatches 219; Indels 156;
                                                                                                                                                                                                                                                                                                                     14.9%; Score 393; DB 9; Length 676; 23.9%; Pred. No. 9.8e-28;
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                            APPLICANT: SCONG, NAY WEI
APPLICANT: STEMMER, WILLEM P.
APPLICANT: POWELL, SHARON K.
APPLICANT: OTTO, EDWARD
TITLE OF INVENTION: STRESS RESISTANT RETROVIRUSES
FILE REPERENCE: 02-107120PC
CURRENT APPLICATION NUMBER: US/09/954,983
CURRENT FILING DATE: 2001-09-17
                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Friend murine leukemia virus
                                                                                                                                 PRIOR APPLICATION NUMBER: 2001-09-17
PRIOR APPLICATION NUMBER: 60/233,398
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 11
LEWARE: PATENTIN Ver. 2.1
 US20020137889A1
                                                                                                                                                                                                                                                                                                                                                      Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Publication No. US20
GENERAL INFORMATION:
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Sequence 8, Application US/09954983; Publication No. US20020137889A1; GENERAL INFORMATION:

US-09-954-983-8

APPLICANT: SCONG, NAY WEI APPLICANT: STEMMER, WILLEM P. APPLICANT: POWELL, SHARON K.

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156 PG-PHRPREAKSCGGPDSFYCASWGCETTGRVYW-----KPSS-----SWDYIT--- 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 IRLKYQNLGPRVPIGPNPVLADQLSFPLPNPQPRPAKSPPASNSTPTLISPSPTPTQPPP 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---APANCSAASQHKLTLSEV-----TGRGLCIGTVPKTHQALCNTTLKTGKGSYYLV 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 PPALTAPPPCCCTTSSS------PYQEFLXRTRLPGN---IDAPSYRSLSKGNSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 TAHTHMPR---NC----YNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 -RTHTRLVSLFNTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 AGTGDRLINLVQGAYQALNFTNPDKTQECWLCLVSGPPYYEGVAV-----LGTYSNHTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.9%; Score 392; DB 9; Length 675;
Best Local Similarity 23.9%; Pred. No. 1.2e-27;
Matches 144; Conservative 77; Mismatches 218; Indels 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Clone ID 2B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 MSDGGGIQGQA------REKQVKEAISQLTRGH----
APPLICANT: OTTO, EDWARD

TITLE OF INVENTION: STRESS RESISTANT RETROVIRUSES
FILE REFERENCE: 02-107120PC
CURRENT APPLICATION NUMBER: US/09/954,983
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/233,398
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.1
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 8
LENGTH: 675
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APPLICANT: SOONG, NAY WEI
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 TAHTHMPR---NC----YNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTS 113
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                                                                                                                                                                                                                                                                                                     14.8%; Score 391; DB 9; Length 672;
24.0%; Pred. No. 1.5e-27;
.ive 75; Mismatches 219; Indels 164;
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APPLICANT: STEMMER, WILLEM P.
APPLICANT: POWELL, SHARON K.
TITLE OF INVENTION: STEESS RESISTANT RETROVIRUSES; FILE REFERENCE: 02-107120PC
CURRENT APPLICATION NUMBER: US/09/954,983
CURRENT FILLING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/233,398
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO FILENGTH: 672
                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                    Matches 145; Conservative
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Clone ID 4-7
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               APPLICANT: SOONG, NAY WEI
APPLICANT: STEWMEN, WILLEM P.
APPLICANT: STEWMEN, WILLEM P.
APPLICANT: OFFICE, SHARON K.
APPLICANT: OFFICE, STEWARD
TITLE OF INVENTION: STRESS RESISTANT RETROVIRUSES
FILLE REFERENCE: 02-107120PC
CURRENT FFLING DATE: 2001-09-17
PRIOR PLING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
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RESULT 29 US-09-954-983-5

RESULT 28 US-09-954-983-6 ; Sequence 6, Application US/09954983 ; Publication No. US20020137889A1

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US-09-954-983-5
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14.7%; Score 386; DB 9; Length 672;
Best Local Similarity 23.9%; Pred. No. 4.5e-27;
Matches 144; Conservative 76; Mismatches 219; Indels 164;
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                                           APPLICANT: SOONG, NAY WEI
APPLICANT: STEWMER, WILLEW P.
APPLICANT: DOWELL, SHARON K.
APPLICANT: OTTO, EDWARD
TITLE OF INVENTION: STRESS RESISTANT RETROVIRUSES
FILE REFERENCE: 02-107120PC
CURRENT APPLICATION NUMBER: 05/09/954,983
CURRENT APPLICATION NUMBER: 60/233,398
PRIOR APPLICATION NUMBER: 60/233,398
PRIOR PILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 14
SOFTWARE PATENTING VET: 2.1
SEQ ID NO 5
Sequence 5, Application US/09954983
Publication No. US20020137889A1
                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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114 MSDGGGIQGQA--------REKQVKEAISQLTRGH------------------ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 AGTGDRILINLVQGAYQALNFTNPDKTQECWLCLVSGPPYYEGVAV-----LGTYSNHTS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 LPSGIFFVCGTSAYHCLNGS----SESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 SSQGWFEGLENR-SPWFTTLISTIMGPLIILLLILLEGPCILNRLVQFVKDRISVVQALV 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 TAHTHMPR---NC----YNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VDNNLTTNQAVKVCKDNKWCNPLAIRFTNTGRQVTSWTTGHYWGLRLYVTGKDPGLTFG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 IRLKYQNLGPRVPIGPNPVLADQLSFPLPNPQPKPAKSPPASNSTPTLISPSPTPTQPPP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---APANCSTASQHKLTLSEV-----TGRGLCIGTVPKTHQALCNTTLKTGKGSYYLV 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 APAGTMWACNTGLTPCLSATVLNRTTDYCVLVELWPRVTYHPPSYVYSOFENSYRHKREP 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 I---LPFVIRAGVLGRLGTGIGSITT---STQFYYKLSQEINGDMEQVTDSLVTLQDQLN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 SLAAVVLQNRRALDILITAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQ 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 NTERW--GLLSQWMPW----VLPFLGPLAALILLLLFGPCIFNLLVKFVSSRIEAVKLQM 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 PG-PHRPREAKSCGGPDSFYCASWGCETTGRVYW-----EPSS-----SWDYIT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 PFALTAPPPCCCTTSSS-----PYQEFLXRTRLPGN---IDAPSYRSLSKGNSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - RIHTRLVSLFNTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Clone ID 2B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.7%; Score 386; DB 9; Length 675; 23.9%; Pred. No. 4.5e-27; ive 76; Mismatches 219; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 VLVGPLVSNLEITHTSNLTCVKFSNTIDTTSSQCIRWVTPPTRIVC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---STPSPYKGLVLSKLHETL
                                                                               APPLICANT: SCONG, NAY WEI
APPLICANT: SCONG, NAY WEI
APPLICANT: STEMMER, WILLEM P.
APPLICANT: STEMMER, WILLEM P.
APPLICANT: OTTO, EDWARD
TITLE OF INVENTION: STRESS RESISTANT RETROVIRUSES
FILE REFERENCE: 02-107120PC
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/233,398
PRIOR APPLICATION NUMBER: 60/233,398
PRIOR PILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.1
Sequence 7, Application US/09954983 Publication No. US20020137889A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 23.9 Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 VLQ 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 7
LENGTH: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-954-983-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661
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Search completed: January 22, 2005, 22:17:05 Job time : 110 secs

5.1.6 Compugen Ltd.		January 22, 2005, 21:17:11 , Search time 39 Seconds
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	using sw model	2005, 21:17:11
Copyright	OM protein - protein search, using sw model	January 22,
	OM protein	Run on:

(without alignments) 1216.279 Million cell updates/sec US-09-319-156B-10 2634 1 MALPYHTELFTVLLPPFALT......KFVSSRIEAVKLQMVLQMEP 493 Title:
Perfect score: Sequence: Scoring table: Run

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	env polyprotein -	env polyprotein -	env polyprotein -	env polyprotein -	env polyprotein pr	retrovirus-related	env polyprotein -	env polyprotein -	env protein - muri	env polyprotein -	env polyprotein -	env polyprotein -	env polyprotein -	env polyprotein pr	env polyprotein -	env polyprotein -	env polyprotein -	env polyprotein -	env polyprotein pr	env polyprotein -	env polyprotein -	env polyprotein -	env polyprotein pr	envelope protein -	env polyprotein -	env polyprotein pr	env polyprotein pr		env polyprotein pr
SUMMARIES	ID	VCMVM7	VCFVAS	VCLJSA	VCLJMP	VCLUHD	B44282	VCVDAR	S12812	T01381	VCVWEM	VCVWFS	A43491	B43491	VCMVPV	VCMVCB	870395	VCVWGF	A25982	VCMVRV	VCVWEK	VCMVLB	VCVWM2	VCMVFP	A46511	VCVWM1	VCMVS2	VCMVSS	T10533	VCMVSA
	DB	-	ч	М		Н	4	٦	~	~	н	Н	7	7	-	н	~	Н	~	-4	, -1	~	-	н	~	-	-	П	~	7
	Length	563	567	587	586	575	570	582	321	9/9	99	989	689	689	919	661	919	662	662	640	699	662	627	668	699	640	642	645	642	639
de	Query Match	22.0	21.2	21.1	20.7	18.1	18.1	17.6	15.8	15.5	15.5	15.3	15.2		14.9	14.9	14.9	14.9	14.9	14.8	14.8	14.8	14.7	14.6	14.6	14.6	14.5	14.5	14.5	14.4
	Score	580	559.5	556	546	477.5	476.5	463.5	415.5	409	407.5	402.5	400	398	393	392.5	392	391.5	391.5	390.5	390	389.5	386	385	385	384	383	383	382	380.5
	Result No.		7	٣	4	S	9	7	80	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

env polyprotein p	env polyprotein pr	env polyprotein pr	env polyprotein -	gp70 protein - mur	env polyprotein -	env polyprotein -	env polyprotein pr	env polyprotein -	env polyprotein -	envelope glycoprot	env polyprotein -	env polyprotein -	envelope glycoprot	env polyprotein -	env polyprotein -
VCMVHL	VCMVVR	VCMVKA	VCMVFG	S15464	S22805	VCMVCE	VCLJGL	A03985	A03986	A45714	VCLJCN	VCLJMT	S14605	VCLJH2	VCVWH
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. 1 999	665 1	665 1	642 1	644 2	353 2	671 1	667 1	201 2	211 2	488 2	488 1	488 1	488 2	486 1	488 1
666 1										8.6 488 2					
666 1	14.4	14.3	14.3	13.9	13.8	13.6	13.6	11.8	11.8	9.8	8.2	7.9	7.9	7.7	7.7

ALIGNMENTS

RESULT 1 VCMVM7 env polyprotein - baboon endogenous NyAlternate names: coat polyprotein NyContains: coat protein gp70; coat C;Species: baboon endogenous virus A;Noce: host Papio sp. (baboon) C;Accession: JT0262 R;Asto, S.; Matsuo, K.; Nishimura, Papin J. Genet. 62, 127-137, 1987 Djm. J. Genet. 62, 127-137, 1987 A;Title: The entire nucleotide seque A;Reference number: JT0260 A;Accession: JT0262 A;Accession: JT0262 A;Accession: JT0262 A;Accession: JT0263 A;Accession: JT0263 A;Genetics: C;Genetics: C;Genetics: coat protein gp70 C;Styperfamily: type C retrovirus env C;Superfamily: coat protein gp70 F;377-563/Product: coat protein p20 F;377-563/Product: coat protein p20 F;377-563/Product: coat protein p312, 312, 312, 312, 312, 312, 312, 312,	RESULT 1 VCMVM7 VALE transport to the baboon endogenous virus (strain M7) VALALernate names: coat polyprotein VALALernate names: coat polyprotein VALALernate names: coat protein gp70; coat protein p20E C;Species: baboon endogenous virus C;Species: baboon endogenous virus C;Species: baboon endogenous virus C;Accession: JT0262 E;Xato, S.; Matsuo, K.; Nishimura, N.; Takahashi, N.; Takano, T. C;Accession: JT0262 A;Yitle: The entire nucleotide sequence of baboon endogenous virus DNA: a chimeric genome A;Reference number: JT0260 A;Accession: JT02
 Ouery Matches 146; Conservative 29.3 Matches 146; Conservative 29.2 Matches 146; Conservative 29.3 Steril Light 1	Query Match 20.0%; Secons 580; DB 1; Length 563; Best Local Similarity 29.2%; Pred. No. 1.5e-36; Best Local Similarity 20.2%; Pred. No. 1.5e-36; Best Local Similarity 20.2%; Pred. No. 1.5e-36; Best Local Similarity 20.2%; Pred. No. 1.5e-36; Best Local Similarity 20.2%; Pred. No. 1.5e-36; Best Local Similarity 20.2%; Pred. No. 1.5e-36; Best Local Similarity 20.2%; Pred. No. 1.5e-36; Best Local Similarity 20.2%; Pred. No. 1.5e-36; Best Local Similarity 20.2%; Pred. No. 1.5e-36; Best Local Similarity 20.2%; Pred. No. 1.5e-36; Best Local Similarity 20.2%; Pred.
 Qy 296 PMTIYT :	296 PMTIYTEQDLYNHVVEKPHNKRVPILPFVIRAGVLGRLGTGGIGSITTSTQFYYKL 350

LGUSVTQYTKL LGEBRCYYVNQ : : : LQEKCCFYVNK LLLLFGPCIFN	Db 448 NDLQDQIDSLAEVYLQNRRGLDLLTAEQGGICLALQEKCCFYANKSGIVRDKIRKLQEDL 507 Qy 426 QCRAEELQNTERWGLLSQWMPWVLPFLGPLAELILLLFGPCIFNLLVFVSRIEAVK 484
LLLTIGPCIFN 530	RESULT 3 VCLJSA WINDSPROTEIN - simian AIDS retrovirus SRV-1 N.Alternate names: coat polyprotein N,Contains: coat protein gp20; coat protein gp70 C;Species: simian AIDS retrovirus SRV-1 A,NOCE: host Macaca mulatta (rhesus macaque) C;Date: 13-Auu-1986 #secuence revision 13-Auu-1986 #text change 16-Jul-1999
vcFvAS env polyprotein - avian spleen necrosis virus NyAlternate names: coat polyprotein NyAlternate names: coat proyectein gp73 NyContains: coat protein gp2; coat protein gp73 C;Species: avian spleen necrosis virus C;Species: avian spleen necrosis virus C;Accession: A38212 R;Kewalramani, V.N.; Panganiban, A.T.; Emerman, M. J;Virol. 66; 3082-3031, 1992 A.Title: Sqleen necrosis virus an avian imminosuppressive retrovirus shares a recentor	C; Accession: A04000 R; Power, M.D.; Marx, P.A.; Bryant, M.L.; Gardner, M.B.; Barr, P.J.; Luciw, P.A. Science 231, 1567-1572, 1986 A; Title: Nucleotide sequence of SRV-1, a type D simian acquired immune deficiency syndron A; Reference number: A94711; MUID:86151668; PMID:3006247 A; Recession: A04000 A; Molecule type: DNA A; Residues: 1-587 < POW> A; Residues: 1-587 < POW> A; Residues: 1-587 < POW> C; Comment: The env nolvarotein contains cost profesin qp20; however.
	C;Genetics: A;Gene: env C;Supericy: type C retrovirus env polyprotein C;Superics: capsid protein; coat protein; dJycoprotein; polyprotein C;Reywords: capsid protein; coat protein; dJycoprotein; polyprotein F;120,237,266,271,277,280,295,308,322,328,340,358,488,585/Binding site: carbohydrate (Asr
ane protein	Query Match Best Local Similarity 29.4%; Pred. No. 1.1e-34; Matches 160; Conservative 84; Mismatches 201; Indels 99; Gaps 17;
Fil-Yul/Pomain: extracellular #status predicted <eal> Fil-Yul/Pomain: extracellular #status predicted <cpl> Fij363-379/Region: hydrophobic #status predicted <cpl> Fij364-397/Region: cleavage processing #status predicted Fij398-567/Product: coat protein gp22 #status predicted <cpl> Fiy08-418/Pomain: transmembrane #status predicted <cpl> Fiy08-418/Pomain: intrancliniar #etatus predicted <tml></tml></cpl></cpl></cpl></cpl></eal>	Qy 19 LTAPPPCCCTT-SSSPYQEFLXRTRLPGNIDAPSYRSLSKG 58 :::
F;245,274,306,328,335/Binding site: carbohydrate (Asn) (covalent) #status predicted Query Match 21.2%; Score 559.5; DB 1; Length 567; Best Local Similarity 31.9%; Pred. No. 5.5e-35; Fair Co. 2007 10.000 10	Db 107ATCYNHYQQCTIGNKTYLTATMIRDKSPSSGDGNVPTILGNNQNLIIAG 155 QY 96 CP-GGLGATVCWTYFTHTSMSDGGGIQGQAREKQVKEAISQLTRGHSTPSPYKGLVLSKL 154
66 THMPRICYNSATLCHHANTHYWTGRAINDSCPGGLGATVCHTYFT 1	155 H-ETLRTHTRINSELENTITERLHEVSAQNPTNCWMCLPLHFREYISIPVPEQWN 115 H-ETLRTHT
QY 111 HTSMSDGGGIQGQAREKQVKEAISQLTRGHSTPS-PYKGLVLSKLHETLRTHTRLVSLFN 169 1	QY 208 NFSTEINTTSVLVGPLVSNLEITHTSNLTCVKFSNTIDTTSSQ 250
QY 170 TTLTRLHEV-SAQNPTNCWMCLPLHFRPYISIPVPEGWNNFSTEI 213 Db :	QY 251 CIRWUTPPTRIVCLPSGIFFVCGTS-AXHCLNGSSESMCFLSFLVPPMTIXTEQD 304 :- :- :-
Qy 214NTTSVLVGPLVSNLEITHTSNLTCVKFSNTIDTTSSQCIRWVTP 257	QY 305 LYNHVVPKPHNKRVPILPFVIRAGVIGRLGTGIGSITTSTQFYXKLSQEINGDMEQVTDS 364
Qy 258 PTRIVCLPSGIFFVCGTS-AYHCLNGSSESMCFLSFLVPPMTIYTEQDLYNHVVPKP 313	QY 365 LVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDR 424 :
314HNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSL 	425 IQCR/ :: 504 LEKR
. Qy 366 VTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRI 425	Qy 485 LQMV 488

provi

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C; Superfamily: type C retrovirus env polyprotein
C; Superfamily: type C retrovirus env polyprotein; polyprotein; transmembrane protein
C; Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane predicted <SIG>P:147/Domain: signal sequence #status predicted <OMP>P:18-386/Product: outer membrane protein #status predicted <TMP>P:387-575/Product: coat protein gp20 #status predicted <TMP>P:387-403/Domain: transmembrane #status predicted <TMI>P:447-481/Region: immunosuppressive peptide
P:518-334/Domain: transmembrane #status predicted <TM2>P:518-334/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted <TM2>P:518-234/Domain: transmembrane #status predicted 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P21412; GB:M23385; NID:g332626; PIDN:AAA66455.1; PID:g332627
C;Genetics:
A;Gene: env
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 ISIPVPEQ-WNNF--STEINTTSVLVGPLVSNLEITHTSNLTCVKFSNTIDTTSSQCIRW 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 SOMHSSCYSSFSQCTQGNNTYFTAILQRTKSTSETNPVTSGLQPHGVLQAGCDGTVGKSV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CWTYFTHTSMSDGGGIQGQAREKQVKEAISQLTRGHSTPSPYKGLVLSKLHETLRTHTRL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---HSEALCPGPGQAFVCGNNLAFTALPANWTGSCVLAALLPDIDIISGDD----PVPIP 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 TFDYIAGRQKRAVTLIPLLVGLGVSTAVATGTAGLGVAVQSYTKLSHQLINDVQALSSTI 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 QCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRIEAV 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: D31827
R; Oda, T.; Ikeda, S.; Watanabe, S.; Hatsushika, M.; Akiyama, K.; Mitsunobu, Virology 167, 468-476, 1988
A; Title: Wolecular cloung, complete nucleotide sequence, and gene structure A; Reference number: A31827; MUID: 89073750; PMID: 3201749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retrovirus-related env polyprotein pseudogene - human
NyAlternate names: coat polyprotein
NyContains: coat protein gp70; coat protein p20E
C;Specise: Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 04-Jan-1996 #text_change 09-Jul-2004
C;Accession B44282
N;Hirose, Y; Takamatsu, M; Harada, F.
                                                                                     N;Contains: coat protein gp20; outer membrane protein
C;Species: squirrel monkey retrovirus SMRV-H
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SCPGGLGATV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 RVQPMPSQVYPCFFKGAQNNSFDIPVG--VANF-----VNCSSSSN---
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monkey retrovirus
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Best Local Similarity 28.5%; Pred. No. 1.1e-28;
Matches 136; Conservative 81; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 THMPRNCYNSATLCMHANTHYWTGKM-----INP---
squirrel
env polyprotein precursor - squirre.
N;Alternate names: coat polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-575 <ODA>
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A; Molecule type: DNA
A; Residues: 1-586 < SONA
A; Residues: 1-586 < SONA
A; Residues: 1-586 < SONA
A; Residues: 1-586 < SONA
A; Cross references: UNIPROT: P07575; GB: M12349; NID: G334702; PIDN: AAA47712.1; PID: G334705
A; Experimental source: clone 6A
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: type C retrovirus env polyprotein
C; Superfamily: type C retrovirus env polyprotein
C; Superfamily: type C retrovirus env polyprotein
C; Superfamily: type C retrovirus env polyprotein
C; Superfamily: capsid protein; glycoprotein; polyprotein
C; Reywords: capsid protein; gp70 #status predicted < GP7>
F; 1-394/Product: coat protein gp70 #status predicted < GP2>
F; 355-586/Product: coat protein gp20 #status predicted < GP2>
F; 205-237, 264, 276, 291, 304, 318, 324, 339, 357, 487/Binding site: carbohydrate (Asn) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-type
                                                                                                                                                                                                                                                                                                      NyAlternate names: coat polyprotein
NyContains: coat protein gp20; coat protein gp70
Sispecies: Mason-Pfizer monkey virus
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: D25839
C;Accession: D25839
S;Sonigo, P.; Barker, C.; Hunter, E.; Wain-Hobson, S.
Cell 45, 375-385, 1986
A;Title: Nucleotide sequence of Mason-Pfizer monkey virus: an immunosuppressive language of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 AONPINCWMCLPLHFRPYISIPVPEQ-WNNFSTEINTTSVLVGP-LVSNLEITHTSNLTC 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461
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Matches 145; Conservative
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AKPI 567
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C; Superfamily: type C retrovirus
C; Keywords: polyprotein
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A;Title: Presence of env genes in members of the RTVL-H family of human endogenous retrons. Reference number: A44282; MUID:93297138; PMID:8517031
A;Accession: B44282
A;Accession: B44282
A;Accession: B44282
A;Accession: B44282
A;Residues: conceptual translation of pseudogene
A;Residues: 1-570 <HR>
A;Residues: 1-570 <HR>
A;Cross-references: UNIPROT:Q9N2K0; GB:D10083
C;Genetics:
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NyAlternate names: coat polyprotein
NyContains: coat protein gp23.
CyGonenic protein gp22; coat protein gp73
CyGonenic avian reticuloendotheliosis virus
CyAccession: A0399
RyMilhelmsen, K.C.; Eggleton, K.; Temin, H.M.
J. Virol. 52, 172-182, 1984
A,Tritle: Nucleotide acid sequences of the oncogene v-rel in reticuloendotheliosis virus
A,Tritle: Nucleotide acid sequences of the oncogene v-rel in reticuloendotheliosis virus
A,Tritle: Nucleotide acid sequences of the strain A,Molecule type: DNA
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; Pred. No. 1.3e-27;
75; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: coat protein; polyprotein; pseudogene F;1-372/Domain: coat protein gp70 <CGP>F;370/Region: opal stop codon F;371-569/Domain: coat protein p20E <CPP>
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C,Superfamily: type C retrovirus env polyprotein
C,Keywords: coat protein; polyprotein
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227 POISDILEATHQVINAINPQLAENCWICGTIGS----POPSRRMAMS----LSMEIA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 LAEVVLQNRRGLDLLTAEQGGICLALQEKCCFYANKSGIVRDKIRKLQEDLLARKRALYD 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LYNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 DSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIR 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GTIQDLÓDQVDSLAEVVLÓNRRGLDLLTAEQGGICLALQEKCCFYANKSGIVRNKIRTLQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 DRIQCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLFGPCIFNLLVKFVSSRIEA 482
                                                                                50 PSYRSLSKGNSTFTAHTHMPRNCYNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYF 109
                                                                                                                                      181
                                                                                                                                                                                              110 THTSMSDGGGIQGQAREKOVKEAISQLTRGHSTPS-PYKGLVLSKLHETLRTHTRLVSLF 168
                                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 VLASLSGATHRVNRCQLLCREADNRTGIPVGYVHFTNCTSIQESLTRRVIYEILRDYVLH 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 SGIFFVCGTSAYHCLNGSSESMCFLSFLVPPWTIYTEQDLYNHVVPKP-----HNKR 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 VPILPFVIRAGVLGRL---GTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNS 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 LAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQN 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            env polyprotein - feline endogenous virus RD114 (fragment)
C;Species: feline endogenous virus RD114
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Sep-1999
C;Accession: S12812
R;Mochring, R.
                                                                                                                                                                                                                                  ----KLLQASCTGIWETSMLGPRCP-----CVC----
                                                                                                                                                                                                                                                                                                             169 NTT----LTRLHEV-SAQNP---TNCWMCLPLHFRPYISIPVPEOWNNFSTEINTTSVLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 SQCIRWVIPPIRIVCLPSGIFFVCGTS-AYHCLNGSSESMCFLSFLVPPMTIYTEQD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 TERWGLLSQWMPWVLPFLGPLAALILLLFGPCIFNLLVKFVSSRIEAVK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 NPLWNGLNGFLPYLLPSLGPLFGLILFLTLGPCIRKTLTRIHDKIQGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 ISIPVPEQWNNFSTEINTTSVLVGP--LVSNLEITHTSNLTCVKFSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.8%; Score 415.5; DB 2; Best Local Similarity 31.2%; Pred. No. 2.8e-24; Matches 96; Conservative 71; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, February 1990 A; Accession: $12812 A; Accession: $12812
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Query Match 15.5%; Score 407.5; DB 1; Best Local Similarity 25.0%; Pred. No. 3e-23; Matches 146; Conservative 77; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 484-662,'CEF' <SUT2>
A;Experimental source: provirus, clone pMLV-201
                                                                                                                                                                                                                                                                                          A, Accession: A93265
A, Molecule type: genomic RNA
A, Residues: 1-665 < SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: A93235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96
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                                                                                                                                                                                                                                                                                                C;Species: murine leukemia virus
C;Species: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01381
C;Accession: T01381
C;Accession: T01381
C;Accession: T01381
A;Tele: Loss of antigenic epitopes as the result of env gene recombination in retroviru A;Reference number: Z14313; MUID:93134803; PMID:7678475
A;Accession: T01381
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-676 <TUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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::| | | | ::|::| | | ::|::| | | | | ::|: | | | ::|: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 TAHTHMPR---NC----YNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFT-HT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMWACNTGLTPCLSATVLNRTTDYCVLVELWPRVTYHPPSYVYSQFEKSHRHKREPVSLT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LALLIGGITMGGIAAGVGTGTTALVATQQFQQLHAAVQDDLKEVEKSITNLEKSLTSLSE 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTER 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 DRLINIVOGAYQALNLTNPDKTQECMLCLVSGPPYYEGVAV-----LGTYSNHTSA--- 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --PANCSVASOHKLTLSEV----TGRGLCIGTVPKTHQALCNTTLKAGKGSYYLVAPTG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPFVIRAGVLGRLGTGIGSITT --- STQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------WDYITVDN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 PFALTAPPPCCCTTS----SSPYQEFLXRTRLPGN---IDAPSYRSLSKGNSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMSDGGGIQGQAREK-----QVKEAISQLTRGH--------
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81; Mismatches 219; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:012374; EMBL:S53043; NID:g263651
C;Genetics:
A;Gene: env
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --STPSPYKGLVLSKLHETL
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2.3e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.5%; Score 409; 23.7%; Pred. No. 2
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env protein - murine leukemia virus
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                                                                                        VKLOMVLO 490
                                                                                                                                             301 VHAMVLAO 308
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replica A;Gene: env (S.Guperfamily: type C retrovirus env polyprotein, spike protein; transmembrane protei: C;Keywords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane protei: B;34-469/Product: knob protein gp70 #status predicted <KNB> F;470-649/Product: spike protein p15E #status predicted <SPK> F;650-665/Product: R protein #status predicted <RPT> F;650-665/Product: R protein #status predicted <RPT> F;45,199,326,358,398,434/Binding site: carbohydrate (Asn) (covalent) #status predicted GB:M76668; NID:g331' A; Experimental source: clone pMLV-1 R; Sutcliffe, J.G.; Shinnick, T.M.; Green, N.; Liu, F.T.; Niman, H.L.; Lerner, R.A. Nature 287, 801-805, 1980 A; Title: Chemical synthesis of a polypeptide predicted from nucleotide sequence allows A; Reference number: A93235, MUID:81052384; PMID:6159543 end reveals details of 21; 211 120 TAHTHMPR---NC----YNSATLCMHANTHYWTGK------MINPSCPGGLGATVC-- 105 -----QGQAREKQVKEAISQLTRGHSTPSPYKGLVLSKLH-ETLRTHTRLVSLFNTTLT 173 PVLADQQPLSKPKPVKSP-----SVTKPPSGTPLSPTQLPPAGTENRLLNLVDGAYQ 323 174 RIHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVGPLVSNLEIT--- 230 LCIGAVPKTHQALC----NTTQTSSRGSYYLVA-----PTGTWWACSTGLTPCISTT 431 PFSSPPGPPCCSGGSSPGCSRDCEEPLTSLTPRCNTAWNRLKLDQTTHKS----NEGFYV 151 NKWCNPLVIRFIDAGRRVTSWTTGHYWGLRLYVSGQDPGLTFGIRLRYQNLGPRVPIGPN 271 -----HISNLTCVKFSNTIDTTSSQCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNGS 283 ----SESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPI---LPFVIRAGVLGRLGTG 336 337 IGSITT----STQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKR 393 ILNLTTDYCVLVELWPRVTYHSPSYVYGLFERSNRHKREPVSLTLALLLGGLTMGGIAAG 491 62 09-Jul-2004 CPGPHRPRESKSCGGPDSFYCAYWGCETTGRAYWKPSSSWDFITVWNNLTSDQAVQVCKD --IDAPSYRSLSKGNSTF--Gaps A; Cross-references: UNIPROT: P03385; GB: J02255; GB: J02256; GB: J02257; Indels 133; Length 665 ---WTYFTHTSMSDGG---GI---env polyprotein - Moloney murine leukemia virus
N;Concains: Knob protein gp70; R protein; spike protein p15E
C;Species: Moloney murine leukemia virus
C;Date: 01-Sep-1981 #sequence revision 24-Sep-1981 #text_change (C;Accession: A93265; A93235; A93288; A03983
C;Accession: A93265; A93235; A93288; A03983
A;Shinnick, T.M.; Lerner, R.A.; Sutcliffe, J.G.
Nature 293, 543-548, 1981
A;Title: Nucleotide sequence of Moloney murine leukaemia virus.
A;Reference number: A93265; MUID:82035843; PMID:6169994 R.A. 'n A; Molecule type: genomic RNA A; Residues: 496-665 <STT1> A; Experimental source: provirus R; Sutcliffe, J.G.; Shinnick, T.M.; Verma, I.M.; Lerner, Proc. Natl. Acad. Sci. U.S.A. 77, 3302-3306, 1980 A; Title: Nucleotide sequence of Moloney leukemia virus: A; Reference number: A93848; MUID:81013872; PMID:6251454 PFALTAPPPCCCTTSS-----SPYQEFLXRTRLPGNò

: : :	SULT 12	•	Forming virus In A A A A A A A A A A A A A A A A A A A	C;Accession: A31668 R;Chattopadhyay, S.K.; Baroudy, B.M.; Holmes, K.L.; Fredrickson, T.N.; Lander, M.R.; Mod C;Superfamily: type C retrovirus env polyprotein C;Reywords: coat protein; glycoprotein; spike protein; transmembrane protein: C;Reywords: coat protein; glycoprotein; spike protein; transmembrane protein: A;Titles Biologic and molecular genetic characteristics of a unique MCF virus that is hit and molecular and molecular protein base. A;Reference unimper A;Reference unimper BB 2: Length 688;	Best Local Similarity 23.7%; Pred. No. 1.2e-22; Matches 141; Conservative 84; Mismatches 215,	Db 111 PFSPPPGPPCCSGSSDSTPGCSRDCEBPLTSYTPRCNTAWNRLKLSKVTH	Keywords: coat protein; glycoprotein; spike protein; transmembrane protein Qy 66 THMPRNCYNSATLCMHANTHYWTGK 90 131-40/Product: knob protein pisE #status predicted <pie> Db 161 AHNEGERYCEGPHRPRWARSCGGPESFYCASWGCETTGRASWRPSSSWDYITVSNNLTSD 220</pie>	us predicted <rpt> tte: carbohydrate (Asn) (covalent) #status predicted Qy 91</rpt>	ength 636; Db 221 QATPACKGNKWCNSLTIRFTSFGKQATSWVTGHWWGLRLYVSGHDPGLIFGIndependent of the control of the co		LGATVCWTYFTHTSMSDGG1000AREK 127 Db 335	191 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPIGPNPVITGQLPPSRPV 250 191 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPIGPNPVITGQLPPSRPV 250 191 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPIGPNPVITGQLPPSRPV 250 192 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPIGPNPVITGQLPPSRPV 250 192 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFTF 270 193 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFTF 270 194 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFTF 270 195 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFTF 270 196 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFTF 270 197 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFTF 270 198 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFTF 270 198 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFTF 270 198 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFT 270 198 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFT 270 198 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFT 270 198 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFT 270 198 AGKKASWDGPKVWGIRLYRSTGIDPVTRFSLTRQVLNIGPRLPGFT 270 198 AGKKASWDGFT 270 198 AGKTASWDGFT 270 198 AGKTASWDGFT 270 198 AGKTASWDGFT 270 198 AGKTASWDGFT 270 198 AGKTASWDGFT 270 198 AGKTASWDGFT 270 198 AGKTASWDGFT 270 198 AGKTASWDGFT 270 198 AGKTASWDGFT 270 198 AGKTASWDGFT 270 198 AGKTASWDGFT 270 1		LTTDYCVLVELWPRVTYHSPS ITTSTOFYYKLSQEINGD	LICVKFSNTIDTISSQCIRWVIPPTRIVCLPSGIFFVCGTSAXHCINGSSESMCFL 290 Db 497	ALCNITORISDGSYLAAPAGTIWACNTGLIPCLSTTVLNLTIDYCVL 413 SPLVPPWITYTEODLYNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTST 344 Db 557 QNRRGLDLLFLKEGGLCAALKEECCFYADHTGLVRDSMAKLRERLSOROKLFESQQGWFE	414 VELMPKVITKISPDYYTQFEFGARFRREPVSLTLALLIGGLINGGIAAGVGTGTTALVAT 473 419 VELMPKVITKISPDYYTQFEFGARFRREPVSLTLALLIGGLINGGIAAGVGTGTTALVAT 473 410 VELMPKVITKISPDYYTQFEFGARFRREPVSLTLALLIGGLINGGIAAGVGTGTTALVAT VASKIEAANLIAL 473 411 VELMPKVITKISPDYYTQFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 412 VELMPKVITKISPDYYTQFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 413 VELMPKVITKISPDYYTQFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 414 VELMPKVITKISPDYYTQFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 415 VELMPKVITKISPDYYTQFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 416 VELMPKVITKISPDYYTQFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 417 VELMPKVITKISPDYYTQFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 418 VELMPKVITKISPDYYTQFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 419 VELMPKVITKISPDYYTQFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 410 VELMPKVITKISPDYYTQFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 410 VELMPKVITKISPDYYTQFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 411 VELMPKVITKISPDYYTGFEFGARFRREPVSLTALLIGGLINGGIAAGVGTGT 673 412 VELMPKTALLIGGLINGGIAAGVGTGT 673 413 VELMPKTALLIGGLINGGIAAGVGTGT 673 414 VELMPKTALLIGGLINGGIAAGVGTGT 673 415 VELMPKTALLIGGLINGGIAAGVGTGT 673 417 VELMPKTALLIGGLINGGIAAGVGTGT 673 417 VELMPKTALLIGGLINGGIAAGVGTGT 673 418 VELMPKTALLIGGLINGGIAAGVGTGT 673 419 VELMPKTALLIGGLINGGIAAGVGTGT 673 410 VELMPKTALLIGGLINGGIAAGVGTGT 673 410 VELMPKTALLIGGLINGGIAAGVGTGT 673 410 VELMPKTALLIGGLINGGIAAGVGTGT 673 410 VELMPKTALLIGGLINGGIAAGVGTGT 673 411 VELMPKTALLIGGLINGGIAAGVGTGT 673 412 VELMPKTALLIGGLINGGIAAGVGTGT 673 412 VELMPKTALLIGGLINGGIAAGVGTGT 673 413 VELMPKTALLIGGLINGGIAAGVGTGT 673 414 VELMPKTALLIGGLINGGIAAGVGTGT 673 415 VELMPKTALLIGGLINGGIAAGVGTGT 673 415 VELMPKTALLIGGLINGGIAAGVGTGT 673 416 VELMPKTALLIGGLINGGIAAGVGTGT 673 417 VELMPKTALLIGGLINGGIAAGVGTGT 673 417 VELMPKTALLIGGLINGGIAAGVGTGT 673 418 VELMPKTALLIGGLINGGIAAGVGTGT 673 418 VELMPKTALLIGGLINGGIAAGVGTGT 673 419 VELMPKTALLIGGLINGGIAAGVGTGT 673 419 VELMPKTALLIGGLINGGIAAGVGTGT 673 410 VELMPKTALLIGGLINGGIAAGVGTGT 673 410 VELMPKTALLIGGLINGGIAAGVGTGT 673 410 VELMPKTALLIGGLINGGIAAGVGTG	CYYVNOSRIVTEKVKEIRDRIOCRAEELONTERWGLLSQWMPWVLPFLGPLAAL
qa	Sy Bp	λ α	RESULT VCVWFS env po N;Alte N;Cont C;Spec	C; Acc R; Cha Virol A; Tit	A, Mol	Sup	7, Key 7,1-3 7,31-	F; 621	Qué Ber Mat	à g	λ	음 음 음	台	& 9G	ठे त	g &	8 & 8	3 &

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C;Accession: B43491
R;Baylac-Kalabokias, H.; Astier-Gin, T.; Moynet, D.; Hernould, M.; Mamoun, R.; Legrand, Virus Res. 18, 117-134, 1991
A;Title: A new leukemogenic retrovirus isolated from tumor cells derived from a radio-in A;Reference number: A43491; MUD:91253260; PMID:2042396
A;Accession: B43491
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-689 <BAY>
                                                                                                                                                                                                                        protei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 ACSTGLTPCISTTILNLTTDYCVLVELWPRVTYHSPSYVYHQFERRAKYKREPVSLTLAL 497
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                                                                                                                                                                                                                                                                                                                                                                         PPSPPPGPPCCSGSNDSTSGCSRDCEEPLTSYTPRCNTAWN-----RLKLSK-----VTH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 AHNEGFYVCPGPHRPRWARSCGGPESFYCASWGCETTGRASWKPSSSWDYITVSNNLTAD 221
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C;Superfamily: type C retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; spike protein;
                                                                                                                                                                                                                                                        Query Match 15.1%; Score 398; DB 2; Length 689; Best Local Similarity 23.5%; Pred. No. 1.7e-22; Matches 140; Conservative 85; Mismatches 215; Indels 156;
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RESULT 14
VGWVPV

VGWVPV

N.Alternate names: coat polyprotein

N.Alternate names: coat polyprotein

N.Alternate names: coat polyprotein

N.Contains: knob protein gp76; R protein; spike protein p15E

C;pccies: Friend murine laukemia virus

C;Date: 31-Mar-1993 murine laukemia virus

C;Date: 31-Mar-1993 murine laukemia virus

C;Accession: A38210; S35476

R;Masuda, M.; Remington, M.P.; Hoffman, P.M.; Ruscetti, S.K.

J. Virol. 66, 2798-2806, 1992

A;Title: Molecular characterization of a neuropathogenic and nonerythroleukemogenic variances number: A38210; MUID:92219364; PMID:1560524

A;Mccession: A38210

A;Melecula type: DNA

A;Residues: 1-676 <SPE>
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spike protein; transmembrane proteir Friend murine leuke PID:9331901 A;Cross-references: EMBL:M91134; NID:g331898; PIDN:AAA46478.1; PID:g331901 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1992 C;Genetics: 63 TAHTHMPR---NC----YNSATLCMHANTHYWTGK-----MINPSCPGGLGATVC-- 105 174 231 383 KLTLSEV-----TGQGLCIGTVPKTHQALCNTTLKTGKGSYYLVAPAGTWMACNTGLT 435 387 275 PVLADQLSFPLPNPLPKPAKSPSASNSTPTLISPSPAPTQPPPAGTGDRLLNLVQGAYQA 334 HCLNGS----SESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPI---LPFVIRAGVL 330 436 PCLSATVLNRTTDYCVLVELWPRVTYHPPSYVYSOFEKSYRHKREPVSLTLALLLGGLTM 495 LLTAKRGGTCLFLGBERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTERW--GLLSQWM 445 556 LLFLKEGGLCAALKEECCFYADHTGLVRDSMAKLRERLTQRQKLFESSQGWFEGLFNR-S 614 PIDN: AAA46478.1; 215 NKWCNPLAIQFTNAGKQVTSWTIGHYWGLRLYVSQQDPGLTFGIRLKYQNLGPRVPIGPN 16 PFALTAPPPCCCTTSSS-----PYQEFLXRTRLPGN---IDAPSYRSLSKGNSTF LHEVSAQNPINCWMCLPLHFRPYISIPVPEQWNN---FSTEINTTSVLVGPLVSNLEITH 335 INLTNPDKTQECWLCL-----VSAPPYYEGVAVLGTYSNHTS---APANCSAGSQH TSNLTCVKFSNT1DTTSSQC1RWVTPPTR1VC-------LPSG1FFVCGTSAY GRLGTGIGSITT---STQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALD 496 GGIAAGVGTGTTALVATQOFQQLHAAVQDDLKEVEKSITNLEKSLTSLSEVVLQNRRGLD A;Cross-references: UNIPROT:P26803; GB:M93134; NID:g331898; PIDN:AAA46. R;Remington, M.P.; Hoffman, P.M.; Ruscetti, S.K.; Masuda, M. Nucleic Acids Res. 20, 3249, 1992. A;Title: Complete nucleotide sequence of a neuropathogenic variant of A;Reference number: S35474; MUID:92319660; PMID:1620621 A;Accession: S35476 A;Reference number: S35476 A;Reference number: S35476 A;Reference number: S35476 A;Reference not shown; translation not shown A;Residues: 1-676 <REM> PW----VLPFLGPLAALILLLFGPCIFNLLVKFVSSRIEAVKLQMVLQ 490 14.9%; Score 393; DB 1; Length 676; 24.1%; Pred. No. 3.9e-22; ive 85; Mismatches 226; Indels 1 134 ----SQLT--RGHSTPSPYKGLVLSKLHETL Best Local Similarity 24.1% Matches 142; Conservative 615 331 셤 g ઠે 8 ò

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A;Cross-references: UNIPROT:P26804; EMBL:Z11128; NID:g61547; PIDN:CAA77479.1; PID:g61549 A;Experimental source: strain FB29 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991 C;Genetics:
                                   MyContains: knob protein gp76; R protein; spike protein p15E
NyContains: knob protein gp76; R protein; spike protein p15E
C;Species: Friend murine leukemia virus
A;Variety: strain FB29
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 870395
Nucleic Acids Res. 19, 6550, 1991
A;Title: Complete nucleotide sequence of Friend murine leukemia virus, strain FB29.
A;Reference number: 870393; MUID: 92107687; PMID: 1762923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SSPYQEFLXRTRLPGN---IDAPSYRSLSKGNSTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPFVIRAGVLGRLGTGIGSITT---STQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: env
C;Superfamily: type C retrovirus env polyprotein
C;Keywords: coat protein; polyprotein; spike protein; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              env polyprotein - feline leukemia virus (strain Gardner-Arnstein)
N;Contains: knob protein gp70; R protein; spike protein p15E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.9%; Score 392; DB 2; L 23.3%; Pred. No. 4.7e-22; ive 81; Mismatches 221;
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les 140; Conservative
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A; Residues: 1-676 <PER>
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C;Genetics:
A;Gene: env
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: type C retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-465/Product: knob protein gp70 #status predicted <KOP>
F;466-661/Product: coat protein p15E #status predicted <PTE>
F;466-661/Product: coat protein p15E #status predicted <PTE>
F;466-61/Product: coat protein p15E #status predicted <PTE>
                                                                                                                                                                                                                                                                                   region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 HFWGLRLYISGHDPGLTFGIRLKVTDLGPRVPIGPNPVLSDQRPPSRPVPARPPPPSASP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||: | :|
|TPTIPPOOG-----TGDRLINLVQGAYLTLNMTDPTRTQECWLCLVSEPPYYE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVAVLREYTSHET------APANCSSGSQHKLTLSEV-----TGQGRCLGTVPKT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TPPT----RIVCLPSGIFFVCGTSAYHCLNGS----SESMCFLSFLVPPMTIY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389 HQALCNRİEPİVSGSNYLVAPEĞILMACSİGLIPCLSTIVLNLITDYCVLVELMPKVIYH 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEQDLYNHVVPKPHNKRVPI --- LPFVIRAGVLGRLGTGIGSITT---STQFYYKLSQEI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIV 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEKVKEIRDRIQCRAEELQNTERW--GLLSQWMPW----VLPFLGPLAALILLLLFGPCI 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627
env polyprotein - Cas-Br-E murine leukemia virus
N;Contains: coat protein pi5E; knob protein gp70 precursor
C;Species: Cas-Br-E murine leukemia virus
C;Species: Cas-Br-E murine leukemia virus
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: B26103
R;Rassart, E; Nelbach, L; Jolicoeur, P.
A;Virol. 60, 910-919, 1986
A;Title: Cas-Br-E murine leukemia virus: sequencing of the paralytogenic reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPDYVYTQFEPGARFRREPVSLTLALLPEGLTMGGIAAGVGTGTTALVATQQFQQLQAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HNDLKEVEKSITNLEKSLTSLSEVVLQNRRGLDLLFLKEGGLCAALKEECCFYADHTGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRLKLARVTHAPKEGF---YICPGSHRPRWA-----RSC-GGLDAYYCASWGCETTGRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 WNPTSSWDYIT-----VSNNLTSSQATKACKNNGWCNPLVIRFTGPGKRATSWTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STPS--PYKGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSAQNPTNCWMCLPLHFRPYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIPVPEOWNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKFSNTIDTTSSOCIRWV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSTFTAH-THMPRNCYNSATLCMHANTHYWTGKMINPSCPGGLGATVC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.9%; Score 322..., 22.8%; Pred. No. 4.2e-22; rive 76; Mismatches 193; Indels 211;
                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A26103; MUID:87061215; PMID:3023680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPYSSPPGPPCCSGDAGAVSGCARDCDEPLTSYSP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 142; Conservative
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A; Residues: 1-661 < RAS>
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A;Title: Localization of neutralizing regions of the envelope gene of feline leukemia vi;
A;Reference number: A25982; MUID:87061257; PMID:2431166
                                             A,Accession: A25982
A,Molecule type: protein
A,Residues: 1-662 <BLD>
A;Cross-references
C,Superfamily: type C retrovirus env polyprotein
C,Keywords: coat protein; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360
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env polyprotein - feline leukemia virus (strain Gardner-Arnstein)
C;Species eline leukemia virus
C;Species 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 09-Jul-2004
C;Accession: A25982
R;Elder, J.H.; McGee, J.S.; Munson, M.; Houghten, R.A.; Kloetzer, W.; Bittle, J.L.; Gran
                                                                                                                                                                                                                                              A;Cross-references: UNIPROT: P03391; GB:K01209; NID:g323910; PIDN:AAA43052.1; PID:g323911
R;Elder, J.H.; McGee, J.S.; Munson, M.; Houghten, R.A.; Kloetzer, W.; Bittle, J.L.; Gran
J. Virol. 61, 8-15, 1987
A;Title: Localization of neutralizing regions of the envelope gene of feline leukemia vi
A;Reference number: A25982; MUID:87061257; PMID:2431166
A;Contents: annotation; peptide synthesis
A;Note: 27 peptides synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: env
C;Superfamily: type C retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane protei
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-465/Product: knob protein gp?0 #status predicted <KPG>
F;466-645/Product: spike protein p15E #status predicted <SKP>
F;466-662/Product: R protein #status predicted <SKP>
F;646-662/Product: R protein #status predicted <SRP>
F;646-662/Product: R protein #status predicted <RRP>
                                                                                                                                       feline leukemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AREKQVKEAISQLTRGHS----TP----SPYKGLVLSKLHETLRTHTRLVSLFN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRQSQIE---SRVTPHHSQGNGGTPGITLVNASIAPLSTPVTPASPKRIGTGDRLINLVQ 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --PSCLSIPQHKLTISEVSGGLCIGTVPKTHQALCNETQQGHTGAHYLAAPNGTYWACN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGLTPCISMAVLNWTSD-FCVLIELWPRVTYHQPBYVYTHFAKAARFRREPISLTVALML 476
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  C;Species: feline leukemia virus
A;Note: host Felis sp. (cat)
C;Date: 10-8ep-1984 #sequence_revision 20-Sep-1984 #text_change 09-Jul-2004
C;Date: 20-8ep-1984 #sequence_revision 20-Sep-1984 #text_change 09-Jul-2004
C;Accession: A03991
R;Nunberg, J.H.; Williams, M.E.; Innis, M.A.
J. Virol. 49; 629-632, 1984
J. Virol. 49; 629-632, 1984
A;Reference number: A92996; MUD:84115095; PMID:6319767
A;Accession: A03991
A;Molecule type: DNA
A;Residues: 1-662 <NUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.9%; Score 391.5; DB 1; Length 662; llarity 27.2%; Pred. No. 5e-22; Conservative 71; Mismatches 158; Indels 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSAYHC-----LNGSSESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPI
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IKQYDP 659
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A;Title: Envelope gene and long terminal repeat determine the different biological proper A;Reference number: A93011; MUID:85237696; PMID:4009793
A;Accession: A03990
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C; Keywords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane protei
C; Keywords: coat protein; glycoprotein; polyproted <SIG>
F;13-3-443/Product: knob protein gp70 #status predicted <KBP>
F;44-640/Product: coat protein p15E #status predicted <PRE>
F;44-640/Product: coat protein p12E #status predicted <PRE>
F;44-623/Product: coat protein p12E #status predicted <PRE>
F;44,58,300,332,339,372,408,576/Binding site: carbohydrate (Asn) (covalent) #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:9332070
                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTERWGLL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 SOWM---PW----VLPFLGPLAALILLILFGPCIFNLLVKFVSSRIEAV-----KLOM 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AREKQVKEAISQLTRGHS----TP-----SPYKGLVLSKLHETLRTHTRLVSLFN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- PSCLSIPQHKLTISEVSGQGLCIGTVPKTHQALCNETQQGHTGAHYLAAPNGTYWACN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQ 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-640 <VOG>
A;Cross-references: UNIPROT:P06445; GB:M10100; NID:g332068; PIDN:AAA46528.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             env polyprotein precursor - Rauscher mink cell focus-forming virus N;Contains: coat protein p12E; coat protein p15E; knob protein gp70 C;Species: Rauscher mink cell focus-forming virus C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                170 TILIRLHEVSAQNPINCWMCLPLHFRPYISIPVPEQWNNFSTEINTISVLVGPLVSNLEI
                                                                                                                                                                                                                                                                                                                                                                                                 316 GTYLALNATDPNRTKDCWLCLVSRPPYYEGIAI---LGNYSNQTNPP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 TSAYHC-----INGSSESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPI-----L
                                                                                                                                 Gaps
                                                                                                                                 81;
spike protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 390.5; DB 1; Length 640;
Pred. No. 5.7e-22;
                                                                    Length 662;
                                                                                                                                 Indels
                                                             Query Match 14.9%; Score 391.5; DB 2; Best Local Similarity 27.2%; Pred. No. 5e-22; Matches 116; Conservative 71; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 THISNLICVKFSNTIDTISSO -- CIRWVTPPTRIVC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Accession: A03990
R; Vogt, M.; Haggblom, C.; Swift, S.; Haas, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    654 IKOYDP 659
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Best Local Similarity
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enviolyprotein - feline leukemia virus (strain lambda-B1) (fragment)
N;Contains: coat protein gp70; coat protein p15E
N;Contains: coat protein gp70; coat protein p15E
C;Species: feline leukemia virus
C;Species: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A27172
R;Nicolaisen-Strouss, K.; Kumar, H.P.M.; Fitting, T.; Grant, C.K.; Elder, J.H.
J. Virol. 61, 3410-3415, 1987
A;Title: Natural feline leukemia virus variant escapes neutralization by a monoclonal ant.
A;Reference number: A27172; MUID:88036192; FMID:2444714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: type C retrovirus env polyprotein
C;Superfamily: type C retrovirus env polyprotein; spike protein; transmembrane proteir
C;Keywords: coat protein; glycoprotein; polyprotein; spike
F;134-465/Product: coat protein gp70 #status predicted <GPS>
F;466-662/Product: coat protein pi5E #status predicted <GPT>
F;466-662/Product: coat protein gi5E #status predicted <GPT>
F;466-662/Product: coat protein gi5E #status predicted <GPT>
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A,Molecule type: DNA
A,Residues: 1-662 «NIC»
A,Cross-references: UNIPROT:P11261, GB:J03448; NID:g323896; PIDN:AAA43048.1; PID:g323897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              552 EGGLCAALKEECCFYADHTGLVRDSMAKLRERLSOROKLFESOOGWFEGLFNK-SPWFTT 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|:| |::| |::| || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 || 315 |
                                                                    --CWTYFTHTSMSDGG---GIQGQAREKQ 128
                                                                                                                                                                                                           -LRTHTRLVSLFNTTL 172
                                                                                                                                                                                                                                                                                   323
                                                                                                                                                                                                                                                                                                                                                                                                    | : | | : | | : | | : | | 324 QALNLTSPDKTQECWLCLVSGPPYYEGVAVLGTYSNHTSAPANCSVASQHKLTLSEVTGQ 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----HISNLTCVKFSNTIDITSSQCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S----SESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPI---LPFVIRAGVLGRLGT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | | : : | | | : | : | : | 432 TILDLTIDYCVLVELWPRVTYHQFERRAKYKREPVSLTLALLLGGLTMGGIAA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392
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144 AHNGGFYVCPGPHRPRWARSCGGPESFYCASWGCETTGRASWKPSSSWDYITVSNNLTSD 203
                                                                                                                                      204 QATPVCKGNEWCNSLTIRFTSFGKQATSWVTGHWWGLRLYVSGHDPGLIFGIRLKITDSG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 GLCIGAVPKTHOVLC----NTTOKTSD------GSYYLAAPTGTTWACSTGLTPCIST 431
                                                                                                                                                                                                                                                                                   264 PRVPIGPNPVLSDRRPPSRPRPTRSPPSNSTPTETPLTLPEPPPAGVENRLLNLVKGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 TRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVGPLVSNLEIT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIGSITT --- STOFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTERW--GLLSQWMPW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 GTYLALNVTNPNKTKDCWLCLVSRPPYYEGIAV---LGNYSNQTNPPPSCLSDPQHKLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THTSNL-TCVKFSNTIDTTSSQCIRWVT---PPTRIVCLPSGIFFVCGTSAYHC----L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -VLPFLGPLAALILLLFGPCIFNLLVKFVSSRIEAVKLQMVLQ 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                              129 VKEAIS----QLTRGHSTPSPYKGLVLSKLHET-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 27.88 Matches 115; Conservative
                                                                    91 MINPSCPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283
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A;Accession: A92995
A;Accession: A92995
A;Accession: A92995
A;Residues: 1-669 cHER>
A;Residues: 1-669 cHER>
A;Cross-references: UNIPROT:P03386; GB:J01998; GB:J01999; GB:K00016; GB:K00017; GB:K0001
A;Cross-references: UNIPROT:P03386; GB:J01998; GB:J01999; GB:K00016; GB:K00017; GB:K0001
B;Herr, W.; Corbin, V.; Gilbert, W.
Nucleic Acids Res. 10, 6911-6944, 1982
A;Title: Nucleotide sequence of the 3' half of AKV.
A;Reference number: A93448; MUID:83090450; PMID:6294621
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C;Keywords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane protei
C;Keywords: coat protein; glycoprotein; polyproteid <SIG>
F;12-11.Domain: signal sequence #status predicted <SIG>
F;32-470/Product: knob protein gp76 #status predicted <KNB>
F;471-650/Product: spike protein pl58 #status predicted <SPK>
F;651-669/Product: R protein #status predicted <RPP:
F;43,199,327,359,399/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEVVLONRRGLDLIFILKEGGLCAALKEECCFYADHTGLVRDSMAKLRERLTQRQKLFESS 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPEGLENR-SPWFTTLISTIMGPLILLLILLEGPCILNRLVQFVKDRISVVQALVLT 626
                                                                                                                                         284 TGDRLLNLVDGAYQALNLTSPDKTQECWLCLVAEPPYYEGVAV-----LGTYSNHTSA- 336
                                                                                                                                                                                                                                                                                   ----PINCSVASQHKLTLSEV-----TGQGLCIGTVPKTHQALCNTTLKTNKGSYYLVAP 387
                                                                                                                                                                                                                                                                                                                                                        SGIFFVCGTSAYHCLNGS----SESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPI- 320
                                                                                                                                                                                                                                                                                                                                                                                                --LPFVIRAGVLGRLGTGIGSITT---STQFYYKLSQEINGDMEQVTDSLVTLQDQLNSL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRIQCRAEELQNT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERW--GLLSQWMPW----VLPFLGPLAALILLLLFGPCIFNLLVKFVSSRIEAVKLQMVL 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFSPPPGPPCCSGSSDSTPGCSRDCEEPLTSYTPRCNTAWN-----RLKLSK-----VTH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TGK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCVWEK
env polyprotein - AKV murine leukemia virus
env polyprotein - AKV murine leukemia virus
N;Contains: knob protein gp76; R protein; spike protein p15E
C;Species: AKV murine leukemia virus
C;Species: 05-Apr-1983 #sequence revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A9295; A93448; A03984
S;Herr, W
J. Virol. 49, 471-478, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THTRLVSLFNTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVL
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       Gaps
       47;
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   Mismatches 146; Indels
                                                                                                                                                                                                              220 VGPLVSNLEITHTSNLTCVKFSNTIDTTSSQCIRWVTPPTRIVC-
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A;Title: Nucleotide sequence of AKV murine leukemia virus.
A;Reference number: A92995; MUID:84115072; PMID:6319746
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A,Molecule type: DNA
A,Residues: 1-34,'R',36-462,'K',464-591,'K',593-669 <HE2>
C,Genetics:
A,Gene: env
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Matches 141;
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Db 373 SEVSGQGSCIGTVPKTHQALCKKTQKGHKGTHYLAAPSGTYWACNTGLTPCISMAVL 429	Db 465 QQPQQLHAAVQDDLKEVEKSITNLEKSLTSLSEVVLQNRRGLDLLFLKERGLCAALKEEC 524
Qy 281 NGSSESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPILPFVIRAGVLGRL 333	Qy 405 CYYVNQSRIVTEKVKEIRDRIQCRAEELQNTERWGLLSQWMPWVLPPLGPLAAL 458
Db 430 NWTSD-FCVLIELWPRVTYHQPEYVYTHFDKTVRLRRRPISLTVALMLGGLTVGGIAAGV 488	525
OY 334 GTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSIAAVVLQNRRALDLLTAKR 393	Qy 459 ILLLEGPCIFNLLVKFVSSRIEAVKLOMVLQ 490 : :
QY 394 GGTCLFLGEBRCYYVNQSRIVTEKVKEIRDRIQCRABELQNTERWGLLSQWM 447	
Qy 448 -VLPFLGPLAALILLLFGPCIFNLLVKFVSSRIEAVKLQMVLQMEP 493 :	env polyprotein precursor (clone CFE-6) - feline leukemia virus (provirus) N;Contains: coat protein pg70; coat protein p15B C;Species: feline leukemia virus A;Note: host Felis silvestris catus (domestic cat) C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
RESULT 22 CUMM2 May WAL	4
W. porpriorent - friend minh. Call locus-locations of the Contains: knob protein gp70; spike protein p15E C;Species: Friend mink cell focus-forming virus C;Date: 20-Sep-1984 #sequence_revision 20-Sep-1984 #text_change 16-Jul-1999	15
.;ACCEBBION: AU3989 KROCh, W.; Zimmermann, W.; Oliff, A.; Friedrich, R. I. Virol, 49. 828-840. 1984	A;kesiques: 1-668 <kum> Cross-references: GB:M25425; NID:g163849; PIDN:AAA30809.1; PID:g163850 C:Genetics:</kum>
4, Title: 17, 120 17, 170 17, 170 17, 170 17, 170 17, 171 18,	Cycancines. A;Gene: env C;Superfamily: type C retrovirus env polyprotein C;Superfamily: type C retrovirus env polyprotein C;Kevwords: coat protein; qlycoprotein; polyprotein; spike protein; transmembrane proteir
A;Molecule type: DNA A;Residues: 1-627 <koc> A;Cross-references: GB:M12528; NID:g331918; PIDN:AAA46483.1; PID:g331920 C;Genetics:</koc>	
y, Gene: env), Superfamily: type C retrovirus env polyprotein), Reywords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane protein), 1-33/Domain: signal sequence #status predicted <sig></sig>	Query Match Best Local Similarity 28.6%; Pred. No. 1.6e-21; Matches 120; Conservative 72; Mismatches 147; Indels 80; Gaps 16;
7:33-431/Product: Knob protein gp/U #Bratus predicted <knb> 7:432-627/Product: spike protein p15E #status predicted <spk> 7:43,58,288,320,360,364,396/Binding site: carbohydrate (Asn) (covalent) #status predicte</spk></knb>	Qy 111 HTSMSDGGGIQGQAREKQVKEAISQLTRGHSTPSPYKGLVLSKLHETLRTHTRLVSLF 168
Query Match 14.7%; Score 386; DB 1; Length 627; Best Local Similarity 25.2%; Pred. No. 1.2e-21; Matches 129; Conservative 79; Mismatches 184; Indels 120; Gaps 17;	169 NTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVGPLVSNLE
QY 54 SLSKGNSTFTAHTHMPRNCYNSATLCMHANTHYWTGKMINPSCPGG	229 ITHTSNLICVKFSNTIDTTSSQCIRWVTPPTRIVC
Qy 100 LGATVCWTYFTHTSMSDGGGIQGQAREKQVKEAISQLTRGHS 141	360RSCLBSVPQHALTISEVSGQGLCIATVPKTHQALCNKIQAGHKGIHXLVAPNGIYMAC 273 GTSAYHCINGSSESMCFLSFLVPPWTIYTEQDLYNHVVPRPHNKRVPILPFVIRA
OY 142TPSPYKGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSAQNPT 184	Db 417 NTGLTPCISMAVLNWTSD-FCVLTELMPRITYHEPEYIYSHFENKPRFKRDPISLTVA 473 Qy 328 GVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAV 378 : : : : : : : : : :
OY 185 NOWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVGPLVSNLEITHISN 234	474 LMLGGITVGGMARNRNRDCGLLETAQFRQLQMAMHTDIQALEESISALEKSLTSLSEV 379 VLQNRRALDLLTAKRGGTCLFLGEBRCYYVNQSRIVTEKVKEIRDRIQCRAEELQNTERW
QY 235 LTCVKFSNTIDTTSSQCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNGSSESMCFL 290	532 VLQNRRGLDILFLQEGGLCTALKEECCFYADHTGLVRDNMAKLRERLKQR-QQLFDSQQI 439 GLLSQWMPWVLPFLGPLAALILLLEGPCIFNLLVKFVSSRIEAVKLQMVLQ
Qy 291 SFLVPPMITYTEQDLYNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTST 344	591 T 24
OY 345 QFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEER 404	A46511 envelope protein - AKV murine leukemia virus C;Species: AKV murine leukemia virus

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transmembrane

#status predicted

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408 TDYCVLVELMPKVTYHSPSYVYGQFEKKKTKYKREPVSLTLALLLGGLTMGGLAAGVGTG 467
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A; Residues: 1-640 cMAR>
A; Cross-references: GB: K02725; NID:g331614; PIDN:AAA46375.1; PID:g331616
A; Experimental Source: clone CI-3
A; Accession: B0387
A; Molecule type: DNA
A; Residues: 1-314,543-640 cMA2>
A; Residues: 1-314,543-640 cMA2>
A; Residues: clone CI-4
C; Superfamily: type C retrovirus env polyprotein; ppike protein; transmemt C; Ksywords: coat protein; glycoprotein; polyprotein; signal sequence #status predicted cSIG>F;31-441/Product: knob protein #status predicted cSIG>F;442/Product: Rpike protein #status predicted cSIP>F;42-621/Product: R protein #status predicted cSPR>F;622-640/Product: R protein #status predicted cSPR>F;43,58,297,329,336,369/Binding site: carbohydrate (Asn) (covalent) #status F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 AGKKASW------DGPKVWGLRLYRSTGTDPVTRFSLTRQVLNIGPRVPIGPNPVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 ITHTSNLTCVKFSNTIDTTSSQCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNGS----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 ESMCFLSFLVPPMIIYTEQDLYNHVVPKPHN-KRVPI---LPFVIRAGVLGRLGTGIGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TT---STOFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.6%; Score 384; DB 1; Length 640; Best Local Similarity 24.7%; Pred. No. 1.8e-21; Matches 128; Conservative 80; Mismatches 187; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLSKGNSTFTAHTHMPRN---CYNSATLCMHANTHYWTGKMINPSCPGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 LGATVCWTYFTHTSMSDGGGIQG------QAREKQVKEAIS----
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C, Genetics:
A, Gene: env
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                                                              Χ.
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                                                              M.; Koseki, H.; Isono,
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N.Contains: knob protein gp70; R protein; spike protein p15E
C;Species: mink cell focus-forming virus
C;Species: mink cell focus-forming virus
C;Date: 20-Sep-1984 #sequence_revision 20-Sep-1984 #text_change 16-Jul-1999
C;Accession: A03987; B0387
A;Nark, G.E; Rapp, U.R.
J, Virol. 49; 530-539, 1984
A;Title: Envelope gene sequence of two in vitro-generated mink cell focus-forming that envelope gene sequence of two in vitro-generated mink cell focus-forming that envelope gene sequence of two in vitro-generated mink cell focus-forming that Recession: A03987; WUID:84115078; PMID:6319752
A;Accession: A03987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | : | : | | 1.4 AHNEGFYVCPGPHRPRWARSCGGPESFYCASWGCETTGRASWKPSSSWDYITVSNNLTSD 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 QATPVCKGNKWCNSLTIRFISFGKQAİSWVIGHWWGLRLYVSGHDPGLIFGİRLKITDSG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- LRTHTRLVSLFNTTL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVGPLVSNLEIT-- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HISNLTCVKFSNTIDTTSSQCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLCIGAVPKTHQVLC----NTTQKTSDGSYYLVA-----PTGTTWACSTGLTPCIST 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S----SESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPI---LPFVIRAGVLGRLGT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIGSITT---STOFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAK 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MINPSCPG----GLGATV----CWTYFTHTSMSDGG---GIQGQAREKQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 PRVPIGPNPVLSDRRPPSRPRPTRSPPPSNSTPTETPLTLPEPPPAGVENRLLNLVKGAY 323
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C; Date: 18-Jun-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 C; Accession: A46511
R; Hayashi, H.; Mateubara, H.; Yokota, T.; Kuwabara, I.; Kanno, M.; Koseki, H. J. Immunol. 149, 1223-1299, 1992
J. Immunol. 149, 1223-1299, 1992
A; Title: Molecular cloning and characterization of the gene encoding mouse m A; Reference number: A46511; MUID: 92364323; PMID: 1380036
A; Accession: A46511
A; Molecule Cype: mRNA
A; Residues: preliminary
A; Molecule Cype: mRNA
A; Residues: 1-669 < HAX>
A; Cross-references: UNIPROT: Q9Q9A5; UNIPROT: Q9DQ24; UNIPROT: Q83382
A; Cross-references: UNIPROT: With the mucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN: 110845, NCBIP: 110846)
C; Superfamily: type C retrovirus env polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                       14.6%; Score 385; DB 2; Length 669;
ilarity 24.3%; Pred. No. 1.6e-21;
Conservative 79; Mismatches 231; Indels 132;
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Matches 142; Conserv
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397

and GA-FeSV

SM-FeSV

env genes of

#text_change 12-Apr-1996

G B

(strain

		Qy 448VLPPLGPLAALILLLEGPCIFNLLVKFVSSRIEAVKLQMVLQMEP 493 : : : :	RESULT 188 T10533 env polyprotein precursor - feline leukemia virus (strain FeLV-FAIDS) env polyprotein precursor - feline leukemia virus N;Contains: env protein gp70; env protein p15E C;Species: feline leukemia virus C;Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T10533 C;Accession: T10533 J;Donahue, P.R.; Hoover, E.A.; Beltz, G.A.; Riedel, N.; Hirsch, V.M.; Overbaugh, J.; Mull J;Virol. 62, 722-731, 1988 A;Title: Strong sequence conservation among horizontally transmissible, minimally pathoge	A; Accession: T10533 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-642 < DON> A; Residues: U-642 < DON> A; Cross-references: UNIPROF: Q85522; EMBL: M18247; NID: g323904; PIDN: AAA93093.1; PIDC; Superfamily: type C retrovirus env polyprotein	Query Match Best Local Similarity 28.2%; Pred. No. 2.6e-21; Batches 106; Conservative 62; Mismatches 144; Indels 64; Gaps 12; Qy 160 THTRLVSLFNTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQNNNFSTEINTTSVL 219 Db 286 TGDRLINLVQGTYLALNATDFNKTKDCWLCLVSRPPYYEGIALLGNYSNQTNPP 339	Qy 220 VGPLVSNLEITHTSNLETCVKFSNTIDTTSSQCIRWYTPPTRIVC	Qy 319 PILPFVIRAGVLGRIGGISITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQ 371 Db 447 PISLTVALMLGGLTVGGIAAGVGTGTKALLETAQF-RQLQMAMHTDIQALEESISALEKS 505 Qy 372 LNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKBIRDRIQCRAEE 431 Db 506 LTSLSEVVLQNRRGLDILFLGEGCCFYADHTGLVRDNMAKLRERLKQRQQL 565	Oy 432 LQNTERWGLLSQWMPWVLPPLGPLALILLLLEGPCIFNLLVKFVSSRIEAV- 483
nily: type C retrovirus env polyprotein coat protein; polyprotein; spike protein; transmemain signal sequence #status predicted <sig> Product: coat protein gp70 #status predicted <gup> Product: coat protein p15E #status predicted <gup> 7,267,302,307,331,334,374,390,410,578/Binding site: carbohydrate (Aatch 28,28; Score 383; DB 1; Length 642; carbohydrate)</gup></gup></sig>	Qy 160 THTRLVSLENTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVL 219	Qy 264 LPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRV 318	Db 447 PISLTVALMIGGITVGGIAAGYGTGTKALLETAQF-RQLQMAMFTDIQALEESISALEKS 505 Qy 372 INSLAAVVLQNRRALDLITAKRGGTCLFLGEBRCYYNQSRIVTEKVKEIRDRIQCRAEE 431 Db 506 LTELSEVVLQNRRALDILFLGEGGLAALKEECCFYADHTGLVRDMAKLRERLKQRQQU 565 Qy 432 LQNTERMGLLSQMMPWVLPFLGPLALLLLLFQFCFRULLVKFVSSRIEAV 483 Db 566 PDSQQGMFEGWFNKSPWFTLISSIMGPLLILLLFGPCILNRLVQFVKDRISVVQ 623	Oy 484KLOMVLOMBP 493 Db 624 ALILTQOYQQIKQYDP 639 RESULT 27	VCMVSS. N. Polyprotein precursor - feline sarcoma virus (strain SM) N.Contains: coat protein gp70; coat protein p15E C; Species: feline sarcoma virus A; Note: host Felis silvestris catus (domestic cat) C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 12-Apr-1996 C; Accession: A33741 R; Guilhot, S.; Hampe, A.; D'Auriol, L.; Galibert, F.	Virology 161, 252-258, 1987 A;Fitle: Nucleotide sequence analysis of the LTRs and env genes of SM-FeSV and GA-FeSV. A;Reference number: A33741; MUID:88044502; PMID:2823466 A;Accession: A33741 A;Molecule type: DNA A;Residues: 1-645 <gui> C;Genetics: A;Genetics:</gui>	C;Superfamily: type C retrovirus env polyprotein C;Kuyevords: coat protein; glycoprotein; polyprotein; spike protein; transmembrane protein F;1-36/Domain: signal sequence #status predicted <sig> F;37-448/Product: coat protein gp70 #status predicted <gup> F;449-645/Product: coat protein p15E #status predicted <guq> F;38,46,61,270,305,310,334,337,377,393,413,581/Binding site: carbohydrate (Asn) (covaler Query Match</guq></gup></sig>	DOCAL SIMILATILY 27.3%; 14; Conservative 7 124 AREKQYKEAISOLTRG 18: : : 253 SROSOTKSKVATOKPOTNG 181 ONPTNCWMCLPLHFRPYIS:

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Search completed: January 22, 2005, 22:13:31
Job time : 42 secs
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everyorder precursor - feline leukemia virus (strain Sarma)

NyAlternate names: coat polyprotein
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NyAlternate names: coat polyprotein
CyBocies: feline leukemia virus
CyBocies: feline leukemia virus
CyBocies: feline leukemia virus
CyBocies: feline leukemia virus
CyBocies: 1-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
CyAccession: A29013
RyAidedel, N.; Hoover, E.A.; Gasper, P.W.; Nicolson, M.O.; Mullins, J.I.
J. Virol. 60, 242-250, 1986
A, Fritle: Molecular analysis and pathogenesis of the feline aplastic anemia retrovirus, feline molecular analysis and pathogenesis of the feline aplastic anemia retrovirus
A,Rocession: A29013
A,Molecule type: DNA
A,Rocession: A29013
A,Molecule type: DNA
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env polyprotein precursor - HoMuLV murine leukemia virus

Ny Contains: knob protein gp76; spike protein p15E

C; Species: HoMuLV murine leukemia virus

A;Note: host Mus hortulanus (European mouse)

C; Date: 3.1-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C; Accession: B32594

R; Voytek, P; Kozak, C.A.

Virology 173, 58-67, 1989

A;Title: Nucleotide sequence and mode of transmission of the wild mouse ecotropic virus,

A;Reference number: A32594; MUID:90051094; PMID:2554579

A;Accession: B32594
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; Pred. No. 3.3e-21;
69; Mismatches 160; Indels 65
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Best Local Similarity 27.6%;
Matches 112; Conservative 6
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A; Molecule type: DNA
A; Residues: 1-666 < VOY>
A; Cross treferences: UNIPROT: P21436
A; Cross treferences: UNIPROT: P21436
A; Note: the authors translated the codon CTT for residue 451 as Pro
C; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Superfamily: type C retrovirus env polyprotein; spike protein; transmembrane protein; C; Keywords: coat protein; glycoprotein; polyprotein; spike protein; glycoprotein; polyprotein; spike protein p15E #status predicted <NGO>
F; A1-466/Product: Knob protein p15E #status predicted <NGO>
F; A1-466/Product: ransmembrane #status predicted <TMI>
F; A1-469/Pomain: transmembrane #status predicted <TMI>
F; GO-320/Domain: transmembrane #status predicted <TMI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 TTHHINGGFYVCPGPHRPRHARNCGGPDDFYCAHWGCETTGQAYWKPSSSWDYIRVSNNA
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241 SNTIDITSSQCIRWVTPPTRIVCLPSGIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIY 300
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                             1825181 seqs, 575374646 residues
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                                               TEQDLYNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQ 360
                                                                             420
                                                                                                    420
                                                                                                                         480
                                                                                                                                    FUNCTION: SU mediates receptor recognition (By similarity).

FUNCTION: TW anchors the envelope heterodimer to the viral membrane through one transmembrane domain. The other transmembrane domain, called fusion peptide, mediates fusion of the viral membrane with the target cell membrane (By similarity).

SUBUNIT: The surface (SU) and transmembrane (TM) proteins form a heterodimer. SU and TM are attached by noncovalent interactions or by a labile interchain disulfide bond (By similarity).

DOMAIN: The CKS-17 immunosuppressive domain is present in many retroviral envelope proteins. As a synthetic peptide, it inhibits immune function in vitro and in vitvo (By similarity).

PTM: Specific enzymatic cleavages in vivo yield the mature SU and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TW proteins (By similarity).

PTM: The CXXC motif is highly conserved across a broad range of retroviral envelope proteins. It is thought to participate to the formation of a labile disulfied bond possibly with the CX6CC motif present in the transmembrane protein (By similarity).

MISCELLANEOUS: Ortholog of the human HERV-W_7q21.1 envelope
                                                                                         VIDSLVILQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKE
                                  TEQDLYNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQ
                                                                             VTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKE
                                                                                                                         IRDRIQCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRI
                                                                                                                                                                                                                                                                                                               [Contains: Surface
                                                                                                                                                                                                                                                                                                                                              Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *IMITARITY: Belongs to the gamma type-C retroviral envelope protein family. ERV class-I W subfamily. CAUTION: CKS-17 sequence does not match the minimal active
                                                                                                                                                                                                                                                                                                  (Envelope
                                                                                                                                                                                                                                                                  05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
ERV-W1 provirus ancstral Env polyprotein precursor polyprotein) (ERVWEL envelope protein) (Syncytin) [Coprotein (SU); Transmembrane protein (TM)].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 QGQAREKQVKEAISQLTRGHSTPSPYKGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 QNPTNCWICLPLDFRPYVSIPVPEERNNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MALPYHTFLFTVLLPPFALTAPPPCCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSKGNS
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                                                                                                                                                                                                                                                                                                                                                                        Potential.
HERV-W1 provirus ancestral Env
polyprotein.
Surface protein (By similarity).
Transmembrane protein (By similarity).
Fusion peptide (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cleavage (By similarity).

CKS-17 (By similarity).

CKGCC (By similarity).

N.linked (GlCNAC...) (Potential).

N.linked (GlCNAC...) (Potential).

N.linked (GlCNAC...) (Potential).

N.linked (GlCNAC...) (Potential).

N.linked (GlCNAC...) (Potential).

N.linked (GlCNAC...) (Potential).
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                                                                                                                                                                                                                                     InterPro; IPR00205, Env polyprotein.
Pfam; PF00429; TLV coat; 1.
Cleavage on pair of basic residues; Envelope protein; ERV;
Glycoprotein; Polyprotein; Signal; Transmembrane;
Transposable element.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1111 (GLCNAC. . .) (Post of 1995 (GLCNAC. ) (Post of 1995) (GLCNAC. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
CXXC (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.6%; Score 2335; DB 1;
89.2%; Pred. No. 4.6e-183;
ive 16; Mismatches 37;
                                                                                                                                                                                     EMBL; AY101588; AAM68167.1; -. EMBL; AY101589; AAM68168.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59939 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 89.2 es 439, Conservative
                                                                                                                                                                                                                                                                                                                                                                          20
538
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409
538 AA;
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-i FUNCTION: 50 mediates receptor recognition (By similarity).
-i FUNCTION: TW anchors the envelope heterodimer to the viral membrane through one transmembrane domain. The other transmembrane domain, called fusion peptide, mediates fusion of the viral membrane with the target cell membrane (By similarity).
-i SUBUNIT: The surface (SU) and transmembrane (TW) proteins form a heterodimer. SU and TM are attached by noncovalent interactions or by a labile interchain disulfide bond (By similarity).
-i-DOMAIN: The CKS-17 immunosuppressive domain is present in many retroviral envelope proteins. As a synthetic peptide, it inhibits immune function in vitro and in vivo (By similarity).
-i-FTW: Specific enzymatic cleavages in vivo yield the mature SU and TW proteins (By similarity).
-i-FTW: Specific enzymatic cleavages in vivo yield the mature SU and TW proteins (By similarity).
-i-FTW: The CXXC motif is highly conserved across a broad range of retroviral envelope proteins. It is thought to participate to the formation of a labile disulfide bond possibly with the CX6CC motif present in the transmembrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pubmed=14757826; DOI=10.1073/pnas.0305763101;
Mallet F., Bouton O., Prudhomme S., Cheynet V., Oriol G., Bonnaud B., Lucotte G., Duret L., Mandrand B., Elucotte G., Duret L., Mandrand B., The endogenous retroviral locus ERVWEI is a bona fide gene involved in hominoid placental physiology.";
Proc. Natl. Acad. Sci. U.S.A. 101:1731-1736(2004).

-I. FUNCTION: Retroviral envelope proteins mediate receptor recognition and membrane fusion during early infection. Endogenous envelope proteins may have kept, lost or modified their original function during evolution. This endogenous envelope protein has retained its original fusogenic properties. In vitro it fuses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells expressing the type D mammalian retrovirus receptors SLC1A4
                                                                                                                                                                                            01-OCT-2004 (Rel. 45, Last annotation update)
ERV-W1 provirus ancestral Env polyprotein precursor (Envelope polyprotein) (ERVWE1 envelope protein) (Syncytin) [Contains: Surface Name=ERVWE1;
                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: Ortholog of the human HERV-W 7q21.1 envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the gamma type-C retroviral envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein family. ERV class-I W subfamily. CAUTION: CKS-17 sequence does not match the minimal active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002050; Env polyprotein.
Pfam; PF00429; TLV coat; 1.
Cleavage on pair of basic residues; Envelope protein; ERV;
Glycoprotein; Polyprotein; Signal; Transmembrane;
                                                                                                                                              538
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EAVKLQMEPKMQ 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9598;
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Q9UQFO; O55244; O9545; Q8NHY7; Q9NRZ2; Q9NZG3;

05-JUL-2004 (Rel. 44, Created)

05-JUL-2004 (Rel. 45, Last sequence update)

01-OCT-2004 (Rel. 45, Last annotation update)

HERV-W 7q21.1 provirus ancestral Env polyprotein precursor (Envelope polyprotein) (HERV-7q Envelope protein) (HERV-7q Envelope protein) (Gyncytin) (Syncytin 1) (Enverin) (Enverin) (Enverin) (Syncytin 1) (Enverin) (Enverin) (Syncytin 2) (Enverin) (Syncytin 1) (Enverin) (Syncytin 2) (Enverin) (Syncytin 3) (Enverin) (Syncytin 4) (Enverin) (Syncytin 5) (Enverin) (Syncytin 6) (Syncytin 70) (Enverin) (Syncytin 70) (Enverin) (Syncytin 70) (Enverin) (Syncytin 70) (Enverin) (Syncytin 70) (Enverin) (Syncytin 70) (Enverin) (Syncytin 70) (Enverin 70) (Enverin 70) (Syncytin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enverin 70) (Enver
                                                                                                                                                               similarity).
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CKS-17 (By similarity).
CKGC (By similarity).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
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                           Potential.
HERV-W1 provirus ancestral Env polyprotein.
Surface protein (By similarity).
Transmembrane protein (By similar Fusion peptide (Potential).
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                                                                                                                                                                                                                                                                CXXC (By similarity)
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88.6%; Pred. No. 4.5e
ive 18; Mismatches
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                                                                                                                                  TFTAHTHMPRNCYNSATLCMHANTHYWTGKMINPSCPGGLGATVCWTYFTHTSMSDGGGI
                                  Gaps
                                  ö
 Length 538;
                                38; Indels
87.9%; Score 2314; DB 1;
88.4%; Pred. No. 2.5e-181;
ive 19; Mismatches 38;
               1 Similarity 88.4 435; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                     480
                  VADSIVTLQDQLNSLAAVVLQNRRALDLLTAERGGTCLFLGEECCYYVNQSGIVTEKVKB 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: SU mediates receptor recognition (By similarity).
FUNCTION: TM anchors the envelope heterodimer to the viral membrane through one transmembrane domain. The other transmembrane domain, called fusion peptide, mediates fusion of the viral membrane with the target cell membrane (By similarity).
SUBDNIT: The surface (SU) and transmembrane (TM) proteins form a heterodimer. SU and TM are attached by noncovalent interactions or by a labile interchain disulfide bond (By similarity).
DOMAIN: The CKS-17 immunosuppressive domain is present in many retroviral envelope proteins. As a synthetic peptide, it inhibits immune function in vitro and in vivo (By similarity).
FTM: Specific enzymatic cleavages in vivo yield the mature SU and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TM proteins (By similarity).

PTM: The CXXC motif is highly conserved across a broad range of retroviral envelope proteins. It is thought to participate to the formation of a labile disulfide bond possibly with the CX6CC motif present in the transmembrane protein (By similarity).

MISCELLANBOUS: Ortholog of the human HERV-W_7Q21.1 envelope
                                                                                     VTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKE
                                                                     IRDRIQCRAEBLQNTERWGLLSQMMPWVLPFLGPLAALILLLFGPCIFNLLVKFVSSRI
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                                                                                                                                                                                                                                                                                                                                                                               Surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

**Bubmed=14757826; DOI=10.1073/pnas.0305763101;

Mallet F., Bouton O., Prudhomme S., Cheynet V., Oriol G., Bonnaud
Lucotte G., Duret L., Mandrand B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Būkaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hylobatidae; Hylobates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the gamma type-C retroviral envelope protein family. BRV class-I W subfamily. CXS-17 sequence does not match the minimal active
                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (Rel. 44, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
ERV-W1 provirus ancestral Env polyprotein precursor (Envelope
polyprotein) (ERVWEI envelope protein) (Syncytin) [Contains: Sprotein (SU); Transmembrane protein (TM)].
                                                                                                                                                                                                                                                                   , 538 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hylobates pileatus (Pileated gibbon)
Eukaryota, Metazoa, Chordata, Crania
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                                                                                                                                             EAVKLOMVLOME 492
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                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Name=ERVWE1
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                                                                                                                                                                     Surface protein (By similarity).
Transmembrane protein (By similarity)
Fusion peptide (Potential).
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(Potential).
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polyprotein.
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CLS-17 (By similarity).
CX6CC (By similarity).
N-linked (GlCNAC. ..) (Pote
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                                                                                                                                                                                                                                                                                  (GlcNAc. . .)
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N-linked (GlcNAc. ..)
                                                                                                                                                                                                                       CXXC (By similarity)
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            or send an email to license@isb-sib.ch)
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entities requires a license agreement
                                  EMBL, AY101592; AAM68171.1; -.
EMBL; AY101593; AAM68172.1; -.
HSSP; P03385; IMOF.
INTEFPC; IPR002050; Env polyprotein.
Pfam; PF00429; TLV_coat; 1.
                                                                                                                                                                                                                                                                                                                                                            60100 MW;
                                                                                                                                                                                                                                                                                                                                                                                   87.8%;
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EAIKLQMEPKME 492
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538 AA;
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RESULT

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-!- FUNCTION: SU mediates receptor recognition (By similarity).
-!- FUNCTION: TM anchors the envelope heterodimer to the viral membrane through one transmembrane domain. The other transmembrane domain, called fusion peptide, mediates fusion of the viral membrane with the target cell membrane (By similarity).
-!- SUBMNIT: The surface (SU) and transmembrane (TW) proteins form a heterodimer. SU and TM are attached by noncovalent interactions or by a labile interchain disulfide bond (By similarity).
-!- DOMAIN: The CKS-17 immunosuppressive domain is present in many retroviral envelope proteins. As a synthetic peptide, it inhibits immune function in vitro and in vivo (By similarity).
-!- PTM: Specific enzymatic cleavages in vivo yield the mature SU and TM proteins (By similarity).
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                                                                                                                                                                                                                                                                                                                                                             Mallet F., Bouton O., Prudhongmes S., Cheynet V., Oriol G., Bonnaud B., Lucotte G., Duret L., Mandrand B.;

Lucotte G., Duret L., Mandrand B.;

"The endogenous retroviral locus ERVWEL is a bona fide gene involved in hominoid placental physiology.";

Proc. Natl. Acad. Sci. U.S.A. 101:1731-1736(2004).

-! FUNCTION: Retroviral envelope proteins mediate receptor recognition and membrane fusion during early infection. Endogenous envelope proteins may have kept, lost or modified their original function during evolution. This endogenous envelope protein has retained its original fusogenic properties. In vitro it fuses cells expressing the type D mammalian retrovirus receptors SLC1A4 and SLC1A5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: The CXXC motif is highly conserved across a broad range of retroviral envelope proteins. It is thought to participate to the formation of a labile disulfide bond possibly with the CX6CC motif present in the transmembrane protein (By similarity).

MISCELLANEOUS: Ortholog of the human HERV-W_7Q21.1 envelope
                                                                                                                  ERV-W1 provirus ancestral Env polyprotein precursor (Envelope polyprotein) (ERVWE1 envelope protein) (Syncytin) (Contains: Surface
                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type-C retroviral envelope
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polyprotein.
Surface protein (By similarity).
                                                                                                                                                                                                          Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelec
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00429; TLV coat; 1.
Cleavage on pair of basic residues; Envelope protein; ERV;
Glycoprotein; Polyprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
PubMed=14757826; DOI=10.1073/pnas.0305763101;
                                                                    05-JUL-2004 (Rel. 44, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update)
538 AA.
                                                                                                                                         polyprotein) (ERVWEl envelope protein) (S;
protein (SU); Transmembrane protein (TM)}
Name=ERVWEl;
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                                                 (Rel. 44, Created)
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
                                                                                                            Score 1528; DB 2;
Pred. No. 4.9e-117;
8; Mismatches 31;
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GO; GO:0019031; C:viral envelope; IEA.
            EMBL; AY050301; AAL11495.1; -
GO; GO:0019031; C:viral envelope; IEA
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
Envelope protein (Fragment).
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Best Local Similarity 87.8%;
Matches 280; Conservative
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similarity).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                               (Potential)
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CXXC (By similarity).

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CX6CC (By similarity).

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01-DEC-2001 (TrEMBLrel. 19, Cre
01-DEC-2001 (TrEMBLrel. 19, Las
01-DEC-2001 (TrEMBLrel. 19, Las
Bruelope protein (Fragment).
Homo sapiens (Human)
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Query Match
Best Local Similarity
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
319 319
319 AA; 35784 MW; 7D288CCCD1B68999 CRC64;
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MEDLINE=21268768; PubMed=11375061;
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MEDLINE=21268768; PubMed=11375061;
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Best Local Similarity 99.4<sup>5</sup>
Matches 179, Conservative
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                                             QNPTNSWMCLPLHFRPXISTPVPEQWNNFSTELLTTSVLVGPLASNVEITHTSNLTCVKF
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submirted (ANG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYOSO293, AALI1493.1;
GO; GO:0019031; C:viral envelope; IEA.
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TEQDLYSYVISKPRNKRVP 319
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TEQDLYSYVISKPRNKRVP 319
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Envelope protein (Fragment)
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Homo sapiens (Human).
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"Human endogenous retrovirus HERV-W family: chromosomal localization,
identification, and phylogeny.";
AIDS Res. Hum. Retroviruses 17:643-648(2001).
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       Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butel
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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EMBL, AB051007; BAB47559.1; -.
GO; GO:0019028; C:viral apsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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99.4%; Pred. No. 2.3e-68;
tive 0; Mismatches 1
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AIDS Res. Hum. Retroviruses 17:643-648(2001)
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"Human endogenous retrovirus HERV-W family: chromosomal localization,
identification, and phylogeny.";
AIDS Res. Hum. Retroviruses 17:643-648 (2001).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Pred. No. 1e-61;
7; Mismatches 9; Indels
                                                                   Query Match 33.0%; Score 870; DB 2; Length 18
Best Local Similarity 92.8%; Pred. No. 2.8e-63;
Matches 167; Conservative 8; Mismatches 5; Indels
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20048 MW; F2B7B2FAF7CE40C3 CRC64;
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Last annotation update)
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91.1%;
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Pfam; PF00429; TLV_coat; 1.
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Matches 164; Conservative
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180 AA;
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MEDLINE=21268768; PubMed=11375061;
Kim H.-S., Lee W.-H.;
"Human endogenous retrovirus HERV-W family: chromosomal localization, identification, and phylogeny.";
AIDS Res. Hum. Retroviruses 17:643-648(2001).
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MEDLINE=21268768; PubMed=11375061;
Kim H.-S., Lee W.-H.;
"Human endogenous retrovirus HERV-W family: chromosomal localization,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 AA; 19471 MW; 70DF3E5658B8E667 CRC64;
                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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90.6%; Pred. No. 5.1e-61;
tive 6; Mismatches 10;
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                                                                                                                                                  Envelope protein (Fragment).
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PRELIMINARY;
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267 GIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPILPFVIR 326
                                                                                                                                                                            327 AGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRAL 386
                                                                                                                                                                                                                       121 AGVLDGLGAGIGGIKTSTQFYYKLSQELNGDMDWYTNSLVTLQDQLNSLAAVVPQNRRAL 180
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MEDILTNE-21268768; PubMed=11375061;
KKIM H.-S., Lee W.-H.;
"Human endogenous retrovirus HERV-W family: chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim H.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
BNBL; ABD50999; BAB47556.1; -.
GO:0019029; C:viral capsid; IEA.
GO: GO:0019031; C:viral envelope; IEA.
GO; GO:00198; F:structural molecule activity; IEA.
InterPro; IRR02050; Bnv polyprotein.
Pfam; PF00429; TLV_coat; 1.
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180 Aa; 19984 MW; 3414BCDD74A060BA CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Envelope protein (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Envelope protein (Fragment).
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AIDS Res. Hum. Retroviruses 17:643-648(2001).
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Q96TB7
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MEDIJUB=21268768; PubMed=11375061;
Kim H.-S., Lee W.-H.;
"Human endogenous retroyirus HERV-W family: chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                         Score 830; DB 2; Length 180;
Pred. No. 5.4e-60;
7; Mismatches 14; Indels
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                                                                                             Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB051009; BAB47561.1; --
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:001901; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
Interepro; IPR02050; Env_polyprotein.
Pfam; PF00429; TLV_Coat; 1.
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB051000; BAB47557.1;
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR002050; Env_polyprotein.
Pfam; PF00422; ILV_coat; 1.
                                                                                                                                                                                                                                                                                                                                                 180 AA; 19709 MW; 4C8F196C9C788497 CRC64;
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19656 MW; EF8DFCBD4CAEAF3D CRC64;
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Last annotation update)
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AIDS Res. Hum. Retroviruses 17:643-648(2001).
       AIDS Res. Hum. Retroviruses 17:643-648(2001)
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Matches 161; Conserv
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SEQUENCE 586 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIFFVCGTSAYRCLNGSSESMCFLSFLVPPWTIYTEQNLYNHVAPKPRNKRVPILPFVIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIFFVCGTSAYHCLNGSSESMCFLSFLVPPMTIYTEQDLYNHVVPKPHNKRVPILPFVIR 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRAL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGVLGGGGGTGGGGTASTQF-YKLSQELNGDMERVADSLVTLQDQLNSLAAVVLQNQTAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 NNFSTEINTTSVLVGPLVSNLEITHTSNLTCVKFSNTIDTTSSQCIRWVTPPTRIVCLPS
                                                                                                                   endogenous retrovirus HERV-W family: chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA stage; Poxviridae; Chordopoxvirinae;
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Singh P., it is a second of isolates from vaccinated Avian Pathol. 29:449-455(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Singh P., Schitzlein W.M., Tripathy D.N.; Shipp P., Schitzlein W.M., Tripathy D.N.; Meticuloendothellosis Virus Sequences Within the Genomes of Strains of Fowlpox Virus Display Variability.";
                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schnitzlein W.M., Singh P., Srinivasan V., Tripathy D.N.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AF246698; AAF81698.2; -. HSSP; P03385; IMOF. GO; GO:0019028; C:viral capsid; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                     15; Indels
                                                                                                                                                                                                       Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                         179 AA; 19228 MW; 3A9FACBAB6376E74 CRC64;
                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      30.3%; Score 797.5; DB 2
87.8%; Pred. No. 2.5e-57;
                                                                                                                               identification, and phylogeny.";
AIDS Res. Hum. Retroviruses 17:643-648(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                     MEDLINE=21268768; PubMed=11375061;
Kim H.-S., Lee W.-H.;
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24,
26,
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01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                      SEQUENCE FROM N.A.
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NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 158;
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AC 091GU
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DT 01-MA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 VQPTGSIDV----NCYAGEADNRTGIPIG-----YVHFTN--CTSIQEVSNETSH--I 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 LPSIEYTAGRHKRAVQFIPLLVGLGITGATLAGGTGLG---VSVHTYHKLSNQLIEDVQA 442
                                                                                                                                                                                                                                                                                                                        TAHTHMPRNCYNSATLCMHANTHYWT------GKMINPSCPGGLGATVCWT 107
                                                                                                                                                                                                                                                                                                                                                      108 YPTHTSMSDGGGIQGQAREKQVKEAISQLTRGHSTPS-PYKGLVLSKLHETLRTHTRLVS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 RNLTR----LCPPPGHVFVCGNNMAYTALPNKWIGLCILASIVPDMSIISGEE----PIP 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 VTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 LDPQTSDILEATHQVLNATNPQLAENCWLCMTLGTPIPAAIPANGNVTLDGNCSLSLPFR 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWVTPPTRIVCLPSGIFFVCGTS-AYHCLNGSSESMCFLSFLVPPMTIYTEQDLYNHVVP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KP-----HNKRVPILPFVIRAGVLGRL---GTGIGSITTSTQFYYKLSQEINGDMEQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRDRIQCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRI 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SO3 LOEDLIARKRALYDNPLWNGLNGFLPYLLPLLGPLFGLIFFLTLGPCIIKTLTRIIHDKI 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Env polyprotein precursor (Coat polyprotein) [Contains: Outer membrane protein GP70; Transmembrane protein p205].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 FRPYISIPVVPEQWNNFSTEI-NTTSVLVGPLVSNLEITHTSNLTCVKFSNTIDTTSSQCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C retroviruses
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                        98;
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                                                                                                                                                                                                                       Length 586;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baboon endogenous virus (strain M7).
Viruses; Retroid viruses; Retroviridae; Mammalian type
NCBI_TaxID=11764;
                                                                                                                                                                    586 AA; 63723 MW; DBB221FA9FC562C3 CRC64;
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR008965; Cellul bind.
InterPro; IPR02050; Env_polyprotein.
Pfam; PF00425; TLV_coat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFNTT---LTRLHEV-SAQNP---TNCWMC------
                                                                                                                                                                                                                  22.3%; Score 588; DB 2; L
32.6%; Pred. No. 1.9e-39;
tive 74; Mismatches 161;
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01-MAR-1989 (Rel. 10, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSPSGPLOE-----CPCN----SYQS-----SVHS----SCYTSYQQCRSGNKTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVKEAISQLTRGHSTPSPYKGLVLSKLHETLRTHTRLVSLFNTTLTRLHEVSAQNPTNCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 MCLPLHFRPYISIPVPEQWNNFSTEI---NTTSVLVGPLVSNLEITHTSNLTCVKFSNTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEEIDLGHVAFSNCTS-ITNVTGPICAVNGSVFLCGNNMAYTYLPTNWTGLCVLATLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRIVTEKVKEIRDRIQCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLFGPCIFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSSPYQEFLXRIRLPGNIDAPSYRSLSKGNSTFTAHTHMPRNCYNSATLCMHANTHYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTS-----SQCIRWVTPPTRIVCLPSGIFFVCGTS-AYHCLNGSSESMCFLSFLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PMTIYTEQD-----LYNHVVPKPHNKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKL
                                                                                                                                                                                                                                                        Outer membrane protein GP70 (Potential)
                                                                              EMBL; D10032; BAA00924.1; -.
EMBL; X05470; CAA29028.1; -.
PIR; JT0262; VCMVM7.
FIRSP; P03385; IMOP.
InterPro; IPR002050; Env polyprotein.
Pfam; PF00429; TLV coat; 1.
Coat protein; Glycoprotein; Polyprotein; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                        (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                   STRAIN=D2/RHE/OR/V1;
MEDLINE=95191045; PubMed=7884914;
Marracid G.H., Kelley R.D., Pilcher K.Y., Crabtree L., Shiigi S.M.,
Avery N., Leo G., Webb M.C., Hallick L.M., Axthelm M.K., Machida C.A.;
"Simian AIDS type D serogroup 2 retrovirus: isolation of an infectious
molecular clone and sequence analyses of its envelope glycoprotein
gene and 3' long terminal repeat.";
J. Virol. 69:2621-2628(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 SVH--SSCYTTYQECFFGNKTYYTAILASNRAPTIGTSNVPTVLGNTHNLLSAGCTGNVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 FALTAPPPCCCTTSSSPYQEFLXRTRLPGNIDAPSYRSLSK------GN---STFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 YVITAPTVYLATVSCSSHTAY-----QPS--DSLKWRCVSNPTLANGENIGNCPCQTFKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KMINPSCPGGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 TRLVSLFNTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-LVSNLEITHTSNLTCV--KPSNT-----IDTTSSQCIRWVTPPTRIVCLPSGIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 PLLVQPLEFINLINASCLYSPFQNNSFGVDVGLVEFINCSTILNI---SHSLCAPNSSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCGTS-AYHCLNGSSESMCFLSFLVPPMT1YTEQDLYNHVVPKP-----HNKR--VPIL
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EMBL, ARI26468, AAD43361.1; -
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002050; Env_polyprotein.
Embl. PF00429; TiV_coat; 1.
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                                                                                                                                                  Betaretrovirus
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                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.5%; Score 567.5; DB 2; 28.5%; Pred. No. 9.1e-38; ive 99; Mismatches 203;
                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 HTHMPRNCYNSATLCMHANTHYWTG--------
                                                                                                                                                  viruses; Retroviridae;
     Created)
                                                                                                                                                                                                                                                                                                                                                                                          ene and 3' long terminal repeat.";
. Virol. 69:2621-2628(1995).
                                                                         Envelope glycoprotein (Fragment)
(TrEMBLrel. 12, (TrEMBLrel. 12, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=D2/RHE/OR/V1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                           Simian retrovirus
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99373443;
                                                                                                                                                                   NCBI_TaxID=39068;
                                                                                                                                                  Viruses; Retroid
01-NOV-1999
01-NOV-1999
                                                  01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Mar.
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372 AIDHYLHRARRAVQFIPLLVGLGITTAVSTGTAGLGYSITQYTKLSRQLISDVQAISSTI 431
                                                                                                                                                                                                                                                                                                                                                                    426 QCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRIEAVKL 485
                                                                                                                                                                                                                                                                                                                                                                                        ---NPS-----CPGGLGA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKLHETLRTHTRLVSLFNTTLTRLHEVSAQNPTNCMMCLPLHFRPYISIPVPEQWNNFST 211
                                                                                                                                                                                         ----SHSLCAPNSSVFVCGNNKAYTYLPSNWTGTCVLATLLPDIDIVPG----DAPVPVP 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 TVCWTYFTHTSMSDGGGIQGQAREKQVKEAISQLTRGHSTPSPYKGLVLSKLHETLRTHT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses.
NCBI_TaxID=11834;
                                                                                                            265 GSNLSCPIIPPLLLVQPLEFMNLINASCFYSPFQNNSFDVDVGLVEFANCSTTLNI----
                                                                                                                                                                                                                                                                                                                    --VKFSNTIDTTSSQCIRW
                                                                                                                                                        255 VTPPTRIVCLPSGIFFVCGTS-AYHCLNGSSESMCFLSFLVPPMTIYTEQDLYNHVVPKP
                                                                                                                                                                                                                             ----HNKR--VPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSL
                                                                                                                                                                                                                                                                                                36 VILLODOLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNOSRIVTEKVKEIRDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLVSLFNTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cosset F.L., Takeuchi Y., Battini J.L., Weiss R.A., Collins M.K.L.; "High titer packaging cells producing recombinant retroviruses resistant to human serum."; J. Virol. 69:7430-7436(1995).

EMBL: X87829; CAA61093.1; -...
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002050; Env polyprotein.
Pfam; PF00429; TLV_coat; 1.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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MEDLINE=96078985; PubMed=7494248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 28.9%
Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPI 554
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SEQUENCE 564 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INPSCPGGLGATVCWTYFTHTSMSDGGGIQGQAREKQVKEAISQLTRGHSTPSPYKGLVL 151
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                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Env polyprotein (Coat polyprotein) [Contains: Coat protein GP70; Coat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCCCT-----TSSSPYQEFLXRTRLPGNIDAPSYRSLSK-----
                                                                                                                                                                                                                                                                                                                                                                                                                          acquired immunodeficiency syndrome.";
Virology 157:317-329(1987).
-!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence relationships of type D retroviruses which cause simian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential).
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Thayer R.M., Power M.D., Bryant M.L., Gardner M.B., Barr P.J.,
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442 SOWMPWVLPFLGPLAALILLLEGPCIFNLLVKFVSSRIEAVKLOMV 488
                   514 HGLLPYLLPLLGPLLCLILLITFGPLFNKIIAFVKQQMDAIQAKPI 560
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Coat protein GP70.
Coat protein GP20.
                                                                                                                                                                                                                                                                                  Viruses; Retroid viruses; Retroviridae; Betaretrovirus
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Pred. No. 2.3e-37;
3; Mismatches 192
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                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                 Simian retrovirus SRV-2.
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                                                                                                                                                      01-OCT-1996 (Rel. 34, 01-OCT-1996 (Rel. 34, 05-JUL-2004 (Rel. 44,
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                                                           PLIVQPMQFSNSSCLSSPFINDTEQIDLGAVFFINCTSVANVSSP---LCALNGSVFLCG 329
                                                                                                                                                                                                                               448
                                                                                                                                                    NNWAYTYLPQNWTRLCVQASLLPDIDINPGDEPVPIPAIDHYIHRP-KRAVQFIPLLAGL 388
                                                                                                                                                                                         387
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                                                                                                              TS-AYHCLNGSSESMCFLSFLVPPMTIYTEQD-----LYNHVVPKPHNKRVPILPFVIRA 327
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STRAIN-Clone PBB101,
MEDLINE=92219390; PubMed=1313915;
Kewalramani V.N., Panganiban A.T., Emerman M.;
"Spleen necrosis virus, an avian immunosuppressive retrovirus, shares a receptor with the type D simian retroviruses.";
J. Virol. 66:3026-3031(1992).
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Coat protein GP73.
Coat protein GP22.
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Viruses: Retroid viruses; Retroviridae; Avian type
NCBI_TaxID=11899;
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polyprotein) [Contains: Coat
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Interpro; IPR02050; Env_polyprotein.
Pfam; PF00429; TLV_coat; 1.
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PIR; A38212; VCFVAS.
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01-JUL-1993 (Rel. 26,
05-JUL-2004 (Rel. 44,
Env polyprotein (Coat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 PIRIVCLPSGIFFVCGTS-AYHCLNGSSESMCFLSFLVPPWTIYTEQDLYNHVVPKP--- 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 ----HNKRVPILPFVIRAGVLGRL---GTGIGSITTSTQFYYKLSQEINGDMEQVTDSL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 OCRABELONTERWGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRIEAVK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508 IERKRALYDNPLWSGLNGFLPYLLPLLGPLFGLILPLTLGPCIMKTLTRIIHDKIQAVK 566
                                                                                                                                                                                                                                                                                                            232 QISDILEATHQVINATNPKLAENCWLCMTL--GTPIPAAIPTNGNVTLDGNCSLSLPFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 YTARRHKRAVQFIPLLVGLGISGATLAGGTGLG---VSVHTYHKLSNQLIEDVQALSGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 THMPRNCYNSATLCMHANTHYWT------GKMINPSCPGGLGATVCWTYFT
                                                                                                                                                                                                                                                                         111 HTSMSDGGGIQGQAREKQVKEAISQLTRGHSTPS-PYKGLVLSKLHETLRTHTRLVSLFN
                                                                                                                                                                                                                                                                                                                                                                                                               170 TT---LTRLHEV-SAQNP---TNCWMCLPLHFRPYISIPVVFEQWN----NFSTEI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 VTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-0CT-1986 (Rel. 02, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Env polyprotein precursor (Coat polyprotein) [Contains: Coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
                                                               93;
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   567;
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Luciw P.A.;
   Length
                                                                   Indels
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21.2%; Score 559.5; DB 1; 31.9%; Pred. No. 4e-37; ive 75; Mismatches 158;
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Pfam; PF00429; TLV_coat; 1.
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HSSP; P03385; 1MOF.
Query Match 21.2
Best Local Similarity 31.9
Matches 153; Conservative
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Simian retrovirus
                                                                                                                                            SEQUENCE FROM N.A. STRAIN=D2/RHE/OR;
                                Viruses; Retroid
NCBI_TaxID=39068;
                                                                                                                                                                                                                                                                     Envelope protein.
                                                                                                                                                              MEDLINE=99373443
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQSRIVTEKVKEIRDR 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQCRAEELQNTERWGLLSQWMPWVLPFLGPLAALILLLLFGPCIFNLLVKFVSSRIEAVK 484
                                                                                                                                                                                                                                                                                                        CPENKKGQVVCWNSQPSVHMSDGGGPQDKVREIIVNKKFEELHKSLFPELSYHPLALPEA
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Polyprotein; Signal; Transmembrane
                                                                                                                                                                                        DB 1; Length 587;
                                                                                                                                                                                       ; Score 556; DB 1; Length 587; Pred. No. 8.1e-37; 84; Mismatches 201; Indel8
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                                                                                                                                                              N-linked (GlcNAc. . .) (Po
80939DD3BFB65A8D CRC64;
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Glycoprotein;
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                                                                                                                                                                                                                                    STRAIN=D2/RHE/OR;
MEDLINE=D5191045; PubMed=7884914;
Marracci G.H., Kelley R.D., Pilcher K.Y., Crabtree L., Shiigi S.M.,
Avery N., Leo G., Webb M.C., Hallick L.M., Axthelm M.K., Machida C.A.;
"Simian AIDS type D serogroup 2 retrovirus: isolation of an infectious
molecular clone and sequence analyses of its envelope glycoprotein
gene and 3' long terminal repeat.";
j. Virol. 69:2621-2628(1995).
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Virology 261:43-58(1999).

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral molecule activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 580;
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                                                                                                                       Betaretrovirus
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                       viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002050; Env_polyprotein.
Pfam; PF00429; TLV_coat; 1.
                         Snvelope glycoprotein (Fragment)
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Best Local Similarity 28.0
Matches 149; Conservative
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162 TRLVSLFNTTLTRLHEVSAQNPTNCWMCLPLHFRPYISIPVPEQWNNFSTEINTTSVLVG 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressive D-type retrovirus.";
Cell 45:375-385(1986).
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HSSP; P03385; 1MOF.
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Marracci G.H., Kelley R.D., Pilcher K.Y., Crabtree L., Shiigi S.M.,
Avery N., Leo G., Webb M.C., Hallick L.M., Axthelm M.K., Machida A.;
"Simian AIDS type D serogroup 2 retrovirus: isolation of an infectious
molecular clone and sequence analyses of its envelope glycoprotein
gene and 3' long terminal repeat.";
J. Virol. 69:2621-2628(1995).
-I- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUJ-2004 (Rel. 44, Last annotation update)
Bnv polyprotein (Coat polyprotein) [Contains: Coat protein GP70; Coat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P03385; 1MOF.
InterPro; IPR002050; Env_polyprotein.
Pfam; PF00429; TLV_coat; 1.
Coat protein; Glycoprotein; Polyprotein; Transmembrane.
CHAIN
S12
CHAIN
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CAA DOACH GP70.
                                                                                                                                                                                                                                                                                                                                             Simian retrovirus SRV-2 (isolate 2R-18B1).
Viruses, Retroid viruses, Retroviridae, Betaretrovirus.
NCBI_TaxID=73490;
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                                                                                                        275 PLLVQPLEFINLINASCLYSPSQNNSFDVDVGLVEFTNCSTTLNI-----SHSLCA 325
219 AQTFNLLTATYSLLNKSNPNLANECWLCLPSGNPVPLAIPS----NDSFLGSNLSCPIIP 274
                                                                ------VKFSNTIDITSSQCIRWVTPPTRIVCL 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501
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                                                                                                                                                                                                PSGIFFVCGTS-AYHCLNGSSESMCFLSFLVPPMT1YTEQDLYNHVVPKP-----HNKR
                                                                                                                                                                                                                                                          326 PNSSVFVCGNNKAYTYLPTNWTGTCVLATLLPDIDIVPG----DAPVFVPAIDHYLHRAR
                                                                                                                                                                                                                                                                                                                             --VPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSLVTLQDQLNSL
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01-AUG-1988 (Rel. 08, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Env polyprotein precursor (Coat polyprotein) [Contains: Coat protein
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MEDLINE=86189951; PubMed=2421920;
SONIGO P., Barker C., Hunter E., Wain-Hobson S.;
"Nucleotide sequence of Mason-Pfizer monkey virus: an
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InterPro, IPR002050; Env polyprotein.
Pfam; PF00429; TLV coat; 1.
Coat protein; Glycoprotein; Polyprotein; Signal.
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(In) Coffin J.M. (eds.);
(In) Coffin J.M. (eds.);
(Cold Spring Harbor Laboratory Press, Cold Spring Harbor. New York, NY, USA (1997).

EMBL; AR033815; AAC82575.1; -...
CHAIN
N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
3CE7A399D9E2F450 CRC64;
                                                                                                                             62;
                                                                                   Length 586;
                                                                                   Score 546; DB 1; Length 58; Pred. No. 5.4e-36; 91; Mismatches 209; Indels
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Viruses, Retroid viruses; Retroviridae; Betaretrovirus.
NCBI_TaxID=11855;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                              62;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 15 days embryo head CDNA, RIKEN full-length enr:
library, clone:D930020E02 product:weakly similar to ENVELOPE
PROTEIN.
                                                          91; Mismatches 209; Indels
   Length
20.7%; Score 546; DB 2; 28.6%; Pred. No. 5.4e-36;
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MEDLINE=99279253; Pubmed=10349636;
Carninol P., Hayashizaki Y.,
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE-21085660; PubMed=11217851;
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SEQUENCE FROM N.A.
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Page 18

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---HNKRVP-ILPFVIRAGVLGRLGTGIGSITTSTQFYYKL 350
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      620 AA
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Pfam; PF00429; TLV coat; 1.
Envelope protein.
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Best Local Similarity 28.1<sup>3</sup>
Matches 134<sup>3</sup>, Conservative
   304 DLYNHVVPKP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 GHRDPYPLSHYQPLTGAALSGQYSVWENEIT-----VQENWDI--TSNI----FSHL 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

C STRAIN=CSPBL/6J; TISSUE=Head;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Fukuda S., Furuno M., Harangaki T., Haraoka T., Hirozane T.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takhahia H., K., Takaku-Akahira S., Takaka Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramateu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/60; TISSUE=Head;

SIDIARE-0550913; Pubmed=11076861;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamotor R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                STRAIN-C57BL/6J; TISSUB-Head;

MEDLINE=20499374; PubMed=11042159;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,

"Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630(2000).
                                                                        of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                              the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60, 770 full-length cDNAs."; Nature 420:563-673(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR002050; Env.polyprotein.
Pfam; PF00429; TLV_coat; 1.
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Best Local Similarity 33.2
Matches 144; Conservative
FANTOM Consortium,
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SEQUENCE 618 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 CYTSTOOCTGKSGTYLTSROORAYGGSTGGDWGPIQISGPTNKYAQASCDKINIGKNVCW 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---VSNLEITHTSNLTCVK---FSNTIDTTSSQCIRW 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 H-----NKRVPILPFVIRAGVLGRLGTGIGSITTSTQFYYKLSQEINGDMEQVTDSL 365
                                                                                        ---NQTVPVPLFASVLSSDSVLRPKRSPHLFPFLAGLGISSALGTGIAGLATSTLYFQQL
                                                           SQEINGDMEQVTDSLVTLQDQLNSLAAVVLQNRRALDLLTAKRGGTCLFLGEERCYYVNQ
                                                                                                                                                                           SRIVTEKVKEIRDRIQCRAEEL-ONTERWGL---LSQWMPWVLPFLGPLAALILLLLFGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 TYFTHTSMSDGGGIQGQAREKQVKEAISQLTRGHSTPSPYKGLVLSK-----LHET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : ::: | | : ::| | 230 IASTHKALNITNPDLAK-----DCWLCMTL-----GTPMPLALLTHDLSFATNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trichosurus vulpecula (Brush-tailed possum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Phalangeridae, Trichosurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baillie G.J., Wilkins R.J.;
"Endogenous type D retrovirus in a marsupial, the common poseum (Trichosurus vulpecula).";
J. Virol. 75:2499-2507[2001].
EMBL; AF284693; AAG28161.1;
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1 (bases 1 to 1329)
Perron,H., Beseme,F., Bedin,F., Paranhos-Baccala,G.,
Komurian-Pradel,F., Jolivet-Reynaud,C. and Mandrand,B.
Isolated nucleotide sequences associated with multiple sclerosis or
rheumatoid arthritis and a process of detecting
Patent: US 6582703-A 108 24-JUN-2003;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1329; Conservative 0; Mismatches
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MIRELLLE SODOYER, CATHERINE OTT, FRANCOIS MALLET, HERVE PERRON, BERNARD MANDRAND (122115/48, C1221/70, C07K14/15, A61K31/70 Strandedness: Single; Topology: Linear; Retroviral nucleic material and nucleotide fragments, in CC
JP 2002509437-A/9
26-MAR-2002
07-JUL-1998 JP 1999508255
07-JUL-1997 FR 97/08816
GLAUCIA PARAHNOS BACCALA, FLORENCE KOMURIAN PRADEL, FREDERIC
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Matches 1329; Conservative 0; Mismatches

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    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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Baccala,G.P., Pradel,F.K., Bedin,F., Sodoyer,M., Ott,C., Mallet,F.,
Perron,H. and Mandrand,B.
Retroviral nucleic material and nucleotide fragments, in
particular, associated with multiple sclerosis and/or rheumatoid
arthritis, for diagnostic, prophylactic and therapeutic uses
Patent: JP 2002509437-A 9 26-MAR-2002;
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TITLE Direct Submission JOURNAL Submitted (16-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA COMMENT On Nov 16, 2001 this sequence version replaced gi:15383820. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doc.gov Finishing Completed at Stanford Human Genome Center www-igi.doc.gov Finishing Completed at Stanford Human Genome Center www-igi.doc.gov Coulity: Phrap Quality >=40 99.8% of Sequence; Bstimated Total Number of Errors is 0.3. FEATURES I. :163803 / Organism="Homo sapiens" / Ab xref="taxon:9606" / Ab xref="taxon:9606" / Colone="RP11-405L7"	Ouery Match Query Match Best Local Similarity 99.3%; Score 1316.4; DB 9; Length 163803; Best Local Similarity 99.3%; Pred. No. 0; Matches 1320; Conservative 0; Mismatches 9; Indels 0; Gaps 0; Qy 1 TCAAAATCGAAGACTTTAGACTTGCTAACCGCCAAAAGAGGGGAACCTGTTTATTTTT 60	241 TTACTCCTTTGACCCTGTATCTTCAACTTCCTTGTTAAGTTTCTCTCCAGAT 300 117364 TTACTCCTCTTTGACCCTGTTTTTTCTCTTCTTCTCTTC	QY 421 AGTCACCCCTCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG 480 Db 117184 AGTCACCCCTCCGAGGAAATCTCAACTGCACACCCCTACTACACTCCCAATTCAGTAGG 117125 QY 481 AAGCAGTTAGAGCAGTTGTCAGCCAACAGTACTTGGGTTTTCCTGTTGAGA 540 Db 117124 AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA 117065 QY 541 GGGTGGACTGAGAGACTAGCTGGATTTCCTAGGCTTATCCTGTTGAGA 117065 Db 117064 GGGTGGACTGAGAGACTAGCTGGATTTCCTAGGCTGACTCAAGACTCCTAAGCCT 117005 QY 601 ANCTGGGAAGGTGACCGACTAGCTGGATTTCCTAGGCTTGAGATCCCTAAGCCT 117005 Db 117004 AGCTGGAAGGTGACCGATCCATTTTAAACATGGCTGACTTAGATCACACCCG 660 Db 117004 AGCTGGAAGGTGACCGATCCATTTTAAACATGGCAAAAACAGGAGTAAACTCACACCCG 116945 QY 661 ACCAATCAGAGACCCATCCATTAAAATGCTAAAAACGGAAAAACAGGAGGTAAAAGCAATAAGCTAAAAACCTAAAAAACGCAAAAAAAA
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1 (Bases I to 10122)

Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TTTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT
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join(247. .811,2872. .9669)

join(247. .811,7440. .9669)

foin(247. .811,7440. .9669)

/product="envelope glycoprotein"

/note="putative mRNA transcript 2"

join(247. .811,9104. .9669)

/note="putative mRNA transcript 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10122;
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89.2%; Pred. No. 0;
iive 0; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="envelope glycoprotein"
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/db_xref="G1:37544416"
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/db_xref="taxon:9600"
/cell_type="PBMC"
/note="isolated_by_PCR;_ERV
                                                                                                                /note="isolated by PCR; i
endogenous_virus: ERV-W"
1. 780
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99512 GCTACTCATTTTTAGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAAT 99571
Direct Submission
Submitted (07-SEP-2002) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
3 (Bases 1 to 148711)
DOB Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Birect Submission
Drive, Walnut Creek, CA 94598, USA
On Nov 28, 2002 this sequence version replaced gi:22758291.
Draft Sequence Produced by DOB Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99392 AATTCGAAATCAAATACAACGTAGAGCAAAAGAGCTTCAAAACGTGGGACACTGAGGCCT
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                                                                                                                                                                                                            www.jgi.doe.gov
Pinishing Completed at Stanford Human Genome Center
Vww-shgc.stanford.edu
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Estimated Total Number of Errors is 0.7.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1067; DB 9;
Pred. No. 0;
0; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                        1. .148711
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="s"
/clone="RP11-120B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.3%;
ilarity 88.9%;
Conservative (
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Best Local Similarity
Matches 1175; Conserv
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DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
TGGGGGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCCTACTAAGAATCCCTAAGCT
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Homo sapiens chromosome 5 clone RP11-120B7, complete sequence
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DOE Joint Genome Institute and Stanford Human Genome Center.
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99511

240

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360

420

99751

480

99811

540

99871

900

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	DOUGH TICHAGETIGECAATCCCCTTGGGTCCCTTGTTTT 100108	0.02 TACCCATTGCCACTCCGATCAGGCTAGCCATTGTTCCTGCATGGCTAAGTGC 10.09 10.0289 CACCCATTGCCATCGGGCTAAAGGCTTGCATTGTTCCTGCAGGCTAAGTGC 10.010289 CACCCATTGCCATCGGGCTAAAAGGCTTGCATTGTTCCTGCAGGTCTGAGTGC 10.0348 10.0000 CTGGGTTTGTCCTAATAGAACTCGATCGGTTCCATGGTTCTCTCCATGA 11.00000 CTGGGTTTGTCCTAATAGAACTGAGTCACTGGTTCTCTTCCATGA 10.00000 10.00000 CTGGGTTCTTAATAGAGCTACTACTCACTGGTTCTTCCTTGT 11.000000 11.0000000000000000000000	Db 100469 ArccGAGAGAGCCAAGAAGAAGAACACGAGGCTTGCCACCATCTTGGAAGTG 100528 Oy 1260 GCCCACTGCCATTTTGGTAGCGGCCCACCATCTTGGGAGCTGTGGGAGCAAGGATCC 1319 Db 100529 GCCCACTGCCATTTTAGAAGTTGCCCACCATCTTAGGAGCTCTAGGAGCAAGGACCC 100588 Oy 1320 CC 1321 Db 100589 CC 100590	AY101591 AY101591 DEFINITION PONGO PYGMAGEUS isolate 1 endogenous retrovirus ERV-W, ERVWE1 locus, allele B, complete sequence. ACCESSION AY101591 AY101691 AY101591 AY101691 A

involved

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LVGPLVSNIEITHTSNLTCVKESNTTYTTNSQCIRWYTPPTQIVCLPSGIFFVCGTSA
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1705. .170
//note="splice acceptor site"
1959. .2694
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                                                                                                                                                                         Z (bases 1 to 2694)
Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2694) Mallet,F. Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G., Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B. The endogenous retroviral locus ERVWEl is a bona fide gene in hominoid placental physiology Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004) 14757826
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Coganisme"Homo sapiens"
/mol type="genomic DNA"
/isolate="individual 132 allele
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/map="7q21-q22"
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/cell_type="PBMC's"
/note="Caucasian
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Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                     AAGCAGTTAGAGCGGTCGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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Maller, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEI is a bona fide gene in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet, F., Bouton, O. and Oriol, G.
Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (JUNN-2002) Retrovirology Department, UMR 2142
CMRS-bloMerieux, Ecole Normale Superieure de Lyon - 46 alle
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers

2 of 2 Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2694)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1036.8; DB 9; Length
Pred. No. 1e-304;
0; Mismatches 110; Indels
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Best Local Similarity 90.2
Matches 1134; Conservative
                                                                                                                                                                                                                     misc_feature
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AF520489S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 22 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence. AF520490.1 GI:33410948

AF520489S2 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

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Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (bordata; Craniata; Vertebrata; Euteleostomi;
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complete cds, and 3' long terminal repeat, complete sequence.
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- 46 allee
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMeriteux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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284. .1900
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1959. .2694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome="7"
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Matches 1134; Conservative
                            AF520506
AF520506.1
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                       ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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                                                                                                                                                        ------CAAATGGAGCCCAAGATGCAGTCCAAGACTAA
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                                  1663 GCTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCCAGAAT
                                                                                                             TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
                                                                                                                                                                                                                        AATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGATGACATTGA
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1602 1482 ä 120 1483 AGGGGAAGAATGCTGTTATTATGTTAATCAATCCGGAATCGTCACTGAGAAAGTTAAAGA 1542 180 240 9 1543 AATTCGAGATCGAATACAACGTAGAGCAGGAGCTTCGAAACACTGGACCCTGGGGCCT 1423 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTATTTTT 61 AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAGTTAAAGA 121 AATTTGAGATCGAATATAATGTAGAGCAGGACCTTCAAAACACTGCACCCTGGGGGCCT 181 CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT 1 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTTTTT 78.0%; Score 1036.8; DB 9; Length 2694; 90.2%; Pred, No. 1e-304; 13;

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> > PRI 11-FEB-2004

AF520505S2 2694 bp DNA linear PRI 11-FEB-2 Homo sapiens individual 37 allele A, envelope glycoprotein gene,

RESULT 10 AF52050582 LOCUS DEFINITION

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78 allele
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/note="splice acceptor site"
1959. .2694
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="PBMC's"
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43. 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284. .1900
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Matches 1134; Conservative
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CCTCAGCCAATGGATGCCCTGGATTCTCCCCTTCTTAGGACCTCTAGGAGCTATAATATT 1662
                                                       AGCTGGGAAGGTGACCACATCTAAACACGGGGCTTGCAACTTAGCTCACACCTG 2070
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                                         241 TTTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT
                                                                                                                                                                                             AGTCACCCCTCCCGAGGAAATCTCAACTGCACACCCCTACTACACTCCAATTCAGTAGG
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RESULT

1 (bases 1 to 2694)
Maller, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004) 1482 AF520529S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 78 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence. 7 120 1483 AGGGGAAGAATGCTGTTATTATGTTAATCAGGAATCGTCACTGAGAAGTTAAAGA 1542 121 AATTTGAGATCGAATATATGTAGAGCAGAGGACCTTCAAAACACTGCACCTGGGGGCCT 180 9 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2694) 1423 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTTTTT AGGGGAAGAATGCTGATAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAAGA TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTT Gaps - 46 allee UMR 2142 DB 9; Length 2694; 13; Score 1036.8; DB 9; Length Pred. No. 1e-304; 0; Mismatches 110; Indels 2 (bases 1 to 2694)
Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (O'JUN-2002) Retrovirology Department,
CMRS-bioMerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France Ā /product="envelope glycoprotein" /protein_id="AAQ17587.1" /db_xref="G1:33411029" ò

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HTRLUSLFNTTTTGLHEVSAQNPTNCWICLPINFRPYVSIPVPEQWINFSTEINTTSV
HVGTVFYNSKLEITHTSNLTCVKFSWTTYTTNSQCIRWYTPPTQTVCLPSGIFFVCGTSA
HCLNGSSESMCFLSFLVPPMTITTEQDLYSYVISGNINFYSTEINTGAGVLGALG
TGTGGITTSTQFYYKLSQEINGDMRRVADSIVTLQPQLNSLAAVLQNRRALDLITAE
RGGTCLFLGEECCYYVNQSGIVTEKVKEIRDRIQRRAEELRNTGPWGLLSQWMPWILP
FLGPLAAIILLLEGPCIFFNLVWFYSSRIBANKLQWEPERMGSKTKIYRRFLDRRPASP
                                                                                                                                                                                                                                                       Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mamalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 2694]

Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,

Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.

The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                 AF520483S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 147 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMeriteux, Escole Normale Superieure de Lyon
d'Italie, Lyon 63364 cedex 07, France
Location/Qualifiers
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/cell_type="PBMC's"
/note="endogenous_virus: HERV-W"
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/mol type="genomic DNA"
/#solate="individual 147 allele
/db xref="taxon:9606"
/chromosome="7"
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/note="splice acceptor site"
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Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                                                                                                            AF520495S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 24 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
                                                                   1141 CCACGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTA 1200
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2694)
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2610 TCCATAAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTTGCCACCATCTTGGGAG 2666
                           2491 TGGGTTCATCCTAATTGAGCTGAACACTAGTCACTGGGTTCCATGGTTCTCTTCTGTGAC
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeriaux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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/organisma"Homo sapiens"
/mol type="genomic DNA"
/isolate="individual 24 allele B"
/db_xref="texon:9606"
/chromosome="7"
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/note="splice acceptor site"
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Homo sapiens (human)
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Query Match 77.9%; Score 1035.2; DB 9; Length 2694; Best Local Similarity 90.1%; Pred. No. 3.1e-304; Matches 1133; Conservative 0; Mismatches 111; Indels 13; Gaps 2; Qy 1 TCAAAATCGAAGAGCTTTAGTTATTGTTAATCAATCTGGAAACAGAGAACCTGTTTATTTT 1482 Qy 61 AGGGAAGAATGCTTATTATTATTAATCAATCTGGAATCGTGAAAAGTTAAAGA 120 Db 1483 AGGGAAGAATGCTTAATTATTGTTAATCAATCGGAATCGTCACTGAGAAAGTTAAAGA 1542 Qy 61 AGGGAAGAATGCTGATAATTATTGTTAATCAATCAGGAATCGTACCTGAGGAAAGTTAAAGA 1542 Db 1483 AGGGAAGAATGCAAATAAAAGAGAGGAGGACCTTCAAAACACTGGACCCTGGGGCCT 180 Db 1543 AATTCGAGATCGAATACAAGAGGAGGAGCTTCGAAACACTGGACCTGGGGCCT 1602 Db 1543 AATTCGAGATCAAAACACTAAGAGGAGGAGCTTCGAAACACTGGACCTGGGGCCT 1602	QY 181 CCTCAGCCAATGGACGCCTGACTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT 240 Db 1603 CCTCAGCCAATGGACCCTGGATTCTCCCCTTCTTAGGACCTCTTAATATTT 1662 QY 241 TTTACTCCTCTTTGGACCCTGATTCTTCAACTTTAAGTTTGTCTCTTCCAGAAT 300 Db 1663 GCTACTCCTCTTTGGACCCTGTATCTTCAAATGGAACCTCTTCAGAAT 1722 QY 301 TGAAGCTGTAAAACTACAAATGGAACCCCAGATGACTCAAATGAATTAATT	0y 541 GGGTGGACTGAGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAGCCT 600 1951 TGGGGACTGAGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCTT 2010 0y 601 ANCTGGGAAGACTGACTGATTTCCTAGGCTGACTTAAGATCCCTAAGCTT 2010 0y 601 ANCTGGGAAGACTCACTCATTTTTAACATGGGGAACTTAGCTCACACCTG 600 0y 601 ANCTGGGAAGACTCACTAAAATGCTAATTAGGAACTTAGCTCACACCTG 2070 0 2011 AGCTGGGAAGACTCACTAAAATGCTAATTAGGAACTTAGCTCACACTG 2070 0 2011 AGCTGGAAGACTCACTAAAATGCTAATTAGGCAAAGAGTAAGCTCACACTG 2070 0 2011 AGCTAATCAGAGACCACACACACACAGGAAAAAAAAAAA

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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordates, Cararrhini, Hominidae, Homo.
1 (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Mallet,F., Lucotte,G., Duret,L. and Mandrand,B.,
The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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TTRLVSLFWTTLTGLHEVSAQNPTWNTCLPLNPRPYVSIPVPEQWNRFSTEINTTSV
LVGPLVSNLEITHTSMLTCVKESNTYTTNSQCIRWTPPPTQLVCCPSGIPFVCGTSA
YRCLNGSSESMCFLSFLVPPMTIYTEQDLYSYVISKPRNKRVPILPFVIGAGVLGALG
                                                                                                                                                                                                                                                                                                                                                                                                                                        AF520503S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 34 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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                                       ACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCC
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                    GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGT
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (O'JUN-2002) Retrovirology Department,
CNRS-bioMerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/mol type="alenomic DNA"
/isolate="individual 34 allele B'
/db_xref="taxon:9606"
/chromosome="7"
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/sex="male"
/cell_type="PBMC's"
/note="endogenous_virus: HERV-W"
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/db_xref="GI.3410977"
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Pred. No. 3.1e-304;
0; Mismatches 111; Indels
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/note="splice acceptor site"
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Homo sapiens individual 45 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
AFF20510
AF520510.1 GI:33410988
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 CTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGTTTGCCACCGGTCACAGACCCGCT
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
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/cell_type="PBMC's"
/note="endogenous_virus: HERV-W"
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/protein_id="AAQ17577.1"
/db_xref="G1:33410989"
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/note="splice acceptor site"
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/mol type="genomic DNA"
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/db xref="taxon:9606"
/chromosome="7"
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/note="syncytin"
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Pred. No. 3.1e-304;
0; Mismatches 111; Indels
                                                     RSDVNDIKGTPPEEISAAQPLLRPNSAGSS"
                                                                       1705. .1720
/note="splice acceptor site"
1959. .2694
                                                                                                                                                                   77.9%;
90.1%;
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Mallet, F. Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF520513S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 49 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence. AF520514
                                                                                                                                                                                                                                                                                                    2491 TGGGTTCATCCTAATTGAGCTGAACACTAGTCACTGGGTTCCATGGTTCTCTTGTGAC 2550
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                 CATGCTATTTCACTCTATTAAATCTTGCAACTGCACTCTTCTGGTCCATGTTTCTTACGG 2310
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 2694)

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                                                                           2311 CTTGAGCTGAGCCTTCGCTCGCCATCCACCACTGCTGTTGCCGCCACCGCAGACCCGCC
                                                                                                                                                                                                                          2431 ACCCATTGCCGCTCCCCAATCGGGCTAAAGGCTTGCCATTGTTCCTGCATGCCTAAGTGCC
                                                      CTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGACCCGCT
                                                                                                                               GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGT
                                                                                                                                                                                                       1021 ACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCC
2 (bases 1 to 2694)
Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/protein_id="AAQ17579.1"
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/isolate="individual 49 allele
/db_xref="taxon:9606"
/chromosome="7"
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/organism="Homo sapiens"
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/note="Asian
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/sex="female"
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YRCLNGSSESWCFLSFLVPPMTIYTTNSQCIRWTPPTQTVCLPGGIFFVCGTSA
TGGGITTSTTGPYYKLSGDLWGPMFTAYDSLVTLODQLNSTRAPULLTAE
RGGTCLFLGEECCYYVKQSGLWGPMFTAYDSLVTLODQLNSTAAVULQNRRALDLLTAE
RGGTCLFLGEECCYYVKQSGTVTEKVKEIRDRIQRRAEELRYTGPWGLLSQNWPWILDF
PLGPLAAIILLLFGPCIFNLLVNFVSSRIEAVKLQMBPKMQSKTKIYRRPLDRPASP
RSDVNDIKGTPPEEISAAQPLLRPNSAGSS"
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//note="splice acceptor site"
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Homo sapiens individual 49 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
AF520516
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Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved
in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 alle
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 2694)
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/isolate="individual 49 allele
/db_xref="taxon:9606"
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2310

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AF520517S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 55 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence. AF520518
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                           AATCATCTATTGCCTGAGAGCACAGCAGGAGGACAATGATCGCGATATAAACCCAAGTC 2190
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2694)
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                                                                                                                                         2191 Trcgagccggcaacgccarcccrrrgggrccccrccrrrgrarggggcrcrgrrr
                                                                                                                                                                                                         CACTCTATTTCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGG
                                                                                                                                                                                                                                                                                                                       CTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTTTTGCCACCGTCACAGACCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGT
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- 46 allee
Maller, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/note="endogenous_virus: HERV-W"
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/mol_type="genomic DNA"
/isolate="individual 55 al
/db xref="taxon:9606"
/chromosome="7"
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/sex="female"
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KEYWORDS
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MIDABSYRSLSKGTPFFTAHTHMPRINTCHASHTYMTGKANTHSCPGGLGV
TVCWTYPTGGRSDGGGGVQDQAREKHYKEVISQLTRVHGTSSPYKGLDLSKLHETLRT
HTRLVSLFNTTLTGLHEVSAQNPTNCWICLPLNFRPYVSIPVPGMNNFSTEINTTSV
LVOPLVSNLEITHTSNLTCVKENTTYTTNSQCTRWTPPFDQTVLTLESGIFFVGGTSA
YRCLNGSSESMCFFLSTLYPPMTIYTTNSQCTRWTPPFDQTVLTCLESGIFFVGGTSA
TGIGGITTSTQPYYKLSQELNGDMERVADSLYTLQDQLNSLAAVVLQNRRALDLLTAE
FGGGTTLFGAECCYYNQSGIYTEKYKRIRDRIQRAAVLQNRRALDLLTAE
FLGPLAAIILLLLLFGFOIFNLLVNFVSSRIEAVKLQMERMENILP
REGDVNDIKGTPPEEISAAQPLLRPNSAGSS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1035.2; DB 9;
Pred. No. 3.1e-304;
0; Mismatches 111;
                                                          /product="envelope glycoprotein"
/protein_id="AAQ17580.1"
/db_xref="GI:33411001"
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/note="splice acceptor site"
1959. .2694
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90.1%;
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Matches 1133; Conservative
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Homo sapiens individual 55 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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1 (Bases I to 2694)

Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.

The endogenous retroviral locus ERWWE1 is a bona fide gene involved proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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2071 ACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCC
                                                               2131 AATCATCTATTGCCTGAGAGCACAGCAGGAGGACAATGATGATGGGTATAAAACCCAAGTC
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 alle
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/chromosome="7"
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                                                                              /codon_start=1
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1 (baess 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Direct Submission
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CNRS-bioMerieux, Bcole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
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/cell_type="PBMC's"
/note="endogenous_virus: HERV-W"
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/note="splice acceptor site"
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/note="syncytin"
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I (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhowme,S., Cheynet,V., Oriol,G., Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (015-Jun-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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TVCLNGSSESGNCFLSPLVPWTYTRQDLYNYVISCARWYTPPTQIVCLPSGIFFVCGTSA
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TGTGGITTSTQFYXKLSQENGDMRRVADSIVTLQDQLNSLAAVVLQNRRALDLLTAE
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FLOPLAAIILLLLFGPCTPTRANLYNTFVSRRIRANTGPWGLLSQWMPWILP
FLOPLAAIILLLLFGPCTPTRANLYNTFVSRRIRANTGPWGLLSQWMPWILP
FLOPLAAIILLLLFGPCTPTRANLYNTFVSRRIRANTGPWGSKTKIYRRPLDRPASP
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0; Mismatches 111; Indels
                                                                                                                                                         43. .57
/note="splice acceptor site"
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/note="splice acceptor site"
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/note="Caucasian
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/note="syncytin"
                                            /map="7q21-q22"
/sex="male"
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AFS20533S2 2694 bp DNA linear PRI 11-FEB-2004
Homo sapiens individual 80 allele A, envelope glycoprotein gene,
complete cds, and 3' long terminal repeat, complete sequence.
AFS20534
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.891 AAGCAGTTAGAGCGGTCGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA 1950
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694)

Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,

Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.

The endogenous retroviral locus ERVWEl is a bona fide gene involve
in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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                                                         ANCTGGGAAGGTGACCGCATCCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCG
                                                                                                                                                                                       ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC
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                                     541 GGGTGGACTGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
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Mallet, F., Bouton, O. and Oriol, G.
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CYMYYFTOTGHBADGGAVGOAREKHWEWISOLTRVHTGRSSPYGGLDSKLHETLRT
HTRLVSLENTTLTGTHBEVSAONPTHOWICLELNKFRPYVSIPVEDRANNFSTEITNTTSV
LVGPLVSNLEITHTSNLTCVKFSNTTYTTNSQCIRWYTPPTQIVCLPSGIFFVCGTSA
YRCLNGSSESWCFLSFLYPPWTIYTTGDLYSYVISKPRNKRYPILPFYIGAGVLGALG
TGIGGITTSTQPYYKLSGLAGDMENVADSLYTLQDQLNSLAAVVLONRRALDLITAE
RGGTCLFLGEBCCYYVNQSGIVTBKVKBIRDRIQGANGLLSQMNWHILP
PLGPLAAIILLLFGGCIFNLLVNFVSSRIEAVKLOMBPKNGSKTKIYRRPLDRPASP
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/map="7q21-q22"
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                                                                                                                                                                                                                                                'note="splice acceptor site"
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                                                                                                                                                   cell type="PBMC's"
country="Brazil"
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AF520336
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1 (bases 1 to 2698)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology
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   1831 AGGCACCCCTCCTGAGGAAATCTCAGCTGCACACCTCTACTACGCCCCCAATTCAGCAGG
                                                            AAGCAGTTAGAGCGGTCGTCGGCCAACCCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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HTRLVSLFNTTLTGLHEVSAQNPTNCWICLPLNFRPYVSIPVPEQWNNFSTEINTTSV
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YRCLNGSSESMCFLSFLVPPMTIYTTSQDLVSYVISKPRNKRVPILPPYIGAGVLGALG
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FLGPLAAIILLLFGPCIFNLLVNFVSSRIEAVKLQMEPKNQSKTKIYRRPLDRPASP
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- 46 allee
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Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
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/chromosome="7"
/map="7q21-q22"
/sex="malle"
/cell_type="PBMC's"
/note="Caucasian
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/note="splice acceptor site"
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    /organism="Homo sapiens"

                                                                            Location/Qualifiers
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AF52053782 2694 bp DNA linear PRI 11-FBB-2004 Complete cds, and 3' long terminal repeat, complete sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2694)
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LNGPLVSNLETTHTSMLTCVKESNTTTNSQCIRWYTPPTOTVCLEGEBEPVCGTSA
YRCLNGSSESMCFLSFLVPPMTYTTNSQCIRWYTPPTOTVCLEGEBEPVCGTSA
TGGGTTTSTQPYYKALSQELNGPMTNTTTNGDLYSTANVTRVPILPFVIGAGUGALG
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FLGPLAALILLLEGEPCIFNLLVNFVSSRIBAVKLQMBPKMQSKTKIYRRPLDRPASP
RSDVNDIKGTPFEELSAAQPLLRPNSAGSS"
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   (6), 1731-1736 (2004)
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                                     2 (bases 1 to 2694)
Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (0-JUN-2002) Retrovirology Department,
CNRS-bioMerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/protein_id="AAQ17590.1"
/db_xref="G1:33411041"
                                                                                                                                                                                                         /mol type="genomic DNA"
/isolate='individual 80 allele
/db xref="taxon:9606"
/chromosome="7"
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/note="splice acceptor site"
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0; Mismatches
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                                                                                                                                                                                             /organism="Homo sapiens"
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/note="Caucasian
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/sex="male"
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Direct Submission
Direct (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene:
In hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
14757826
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                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/isolate="individual 81 allele
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/note="splice acceptor site"
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Homo sapiens individual 95 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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                                                                                                                                                                                                                                                    1891 AAGCAGTTAGAGCGGTCGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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Homo sapiens individual 96 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.

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             301 TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
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                                                                                                                      <u> AATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA</u>
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694).
Mallet,F., Bouton,O., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMerstaux, Escale Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/note="endogenous_virus: HERV-W"
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/mol type="genomic DNA"
/isolate="individual 95 allele
/db xref="taxon:9606"
/chromosome="7"
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/note="splice acceptor site"
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AF520561S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 71 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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                                                      TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
                                                                                                                         AATCTACCGTGGACCCCTGGCCGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA
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1 (Bases I to 268)
Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEI is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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YRCLNGSSESMCFLSFLVPPMTIYTTGDLYSYVISKPRNKRVPILPFVIGAGVLGALG
TGIGGITTTSTQFYXKLSQELMODMERYNDSLYTLQDQLNSLAAVVLQNRRALDLLTAE
RGGTCLFLGEECCYYVUGSGIVTEKVKEIRDRIQRRABELRNTGPWGLLSGWMPWILP
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Direct Submission
Submitted (O7-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/sex="male"
/cell_type="PBMC's"
/note="endogenous_virus: HERV-W"
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/chromosome="7"
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                                                                                                                                       Eukaryoff, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEI is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
14757826
2 (bases I to 2694)
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Direct Submission
Submitted (O'JUN-2002) Retrovirology Department, UMR 2142
CMRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
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/note="splice acceptor site"
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/note="splice acceptor site"
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       AF520562
AF520562.1 GI:33411092
                                                                                              Homo sapiens (human)
Homo sapiens
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Matches 1133; Conservative
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Job time : 5585.86 secs

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GenCore version 5.1.6
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January 22, 2005, 11:11:14 ; Search time 609.913 Seconds (without alignments) 11438.492 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-319-156B-12 1329 Title: Perfect score:

1 tcaaaaatcgaagagctttag.......gcaaggatcccccagtaaca 1329 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

8269772 Total number of hits satisfying chosen parameters: 4134886 segs, 2624710521 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001as:*
6: geneseqn2001bs:*
7: geneseqn2002bs:*
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9: geneseqn2003bs:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		* Ouery				
No.	Score	Match	Length	BB	ID	Description
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0	1326	99.8	1329	0	AAX29704	Aax29704 Clone 5M6
М	1326	99.8	1329	12	ADG14849	Adg14849 MSRV asso
4	1299	7.76	1329	6	ADB84403	Adb84403 MSRV-1 as
S	1035.2	77.9	56093	9	ABL61744	Ab161744 Colon ade
9	1029.4	77.5	9502	10	ADF59718	Adf59718 Human con
7	1023.2	77.0	10499	က	ABN97929	Abn97929 Human ret
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14	731.8	55.1	2946	m	AAZ59468	Aaz59468 Human sec
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17	730.2	54.9	2781	ß	AAF55630	Aaf55630 Nucleotid
18	728.6	54.8	6394	ស	AAS84210	Aas84210 DNA encod
19	722.6	54.4	7582	7	AAX25665	Aax25665 Complete
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Aaa59210 3' pol ge	Aax25661 Human end	Aaa59211 5' non co	Aah20069 HERV-W en	Aai14608 Probe #45	Aba56337 Human foe	Probe		Aba25978 Probe #44	Aak30018 Human bon	Aak04516 Human bra	Abs29670 Human liv	Aai04422 Probe #44	Abs04589 Human gen	Aas77313 DNA encod	Aas65964 DNA encod	Abn97978 Human ret	Aax25669 Human end	Ade09587 Novel DNA	Abn97930 Human ret	Ado47194 DNA segue	Abn97947 Human ret	Acc84313 Human ear	Abn97946 Human ret
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721.2	712.6	712.6	712.6	704.8	704.8	704.8	704.8	704.8	704.8	704.8	704.8	704.8	704.8	680.6	651	643.4	639.8	610.4	607	601.4	596.8	593.6	580.6
22	23	24	25	56	27	28	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

codon) // cransl_except= (pos:125-127, appears to code for a stop codon) /transl_except= (pos:137-139, appears to code for a stop codon) Multiple sclerosis associated retrovirus; MSRV; MS; pol gene; gag gene; env gene; rheumatoid arthritis-associated virus; ss. /*tag= a /product= "Encodes protein AAW71069" /transl_except= (pos:77-79, appears to code for a stop Multiple sclerosis associated retrovirus fragment 6. Multiple sclerosis associated retrovirus. Location/Qualifiers 2. .490 AAV43219 standard; cDNA; 1329 BP. 97WO-IB001482. 29-DEC-1998 (first entry) WO9823755-A1 26-NOV-1997; 04-JUN-1998. AAV43219; RESULT 1 AAV43219 Key

96US-00756429. (INMR) BIO MERIEUX 26-NOV-1996;

Perron H, Beseme F, Bedin F, Paranhos-Baccala Komurian-Pradel F, Jolivet-Reynaud C, Mandrand

0 0

WPI; 1998-322732/28. P-PSDB; AAW71069.

New nucleic acid from retroviruses - useful for diagnosis, prevention and treatment of, e.g. multiple sclerosis.

Aax25660 Human end

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841 CACTCTATTTCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGG
                                                                                                       CTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGACCCGCT
                                                                                                                           901 CTCAAGCTGAGCTTTTGTTCGCCATCCACCACCACTGCTGTTTGCCACCGTCACAGACCCGCT
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                                              The present sequence represents a multiple sclerosis (MS) associated retrovirus (MSRV) genomic fragment used in the method of the invention. The invention provides complete or partial sequences of the MSRV-1 pol gene, gag gene and env gene, and polypeptides encoded by these genes. The invention also provides antibodies raised against the pulpaptides. The genomic sequences, polypeptides and antibodies are also claimed useful for diagnosing infection by MS and rheumatoid arthritisassociated viruses, and also for prevention and treatment of infection
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Komurian-Pradel F, J
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26-NOV-1997;
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          This sequence represents clone 5M6 from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-ANG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
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useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis. The present sequence is used in the exemplification of the invention.
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         The invention relates to an isolated or purified nucleic acid from a virus associated with multiple sclerosis and/or rheumatoid arthritis, antitiple sclerosis-associated virus (MSRV):1. The nucleic acids comprise pol, gag or reverse transcriptase genes (or their fragments) encoding the proteins or defined peptides (including immunodominant peptides.

CC detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample, a nucleic acid probe for the detection of a virus associated with multiple sclerosis or rheumatoid arthritis, a primer for the amplification by polymerisation of a nucleic acid of a viral material associated with multiple sclerosis or rheumatoid arthritis, a cr viral material associated with multiple sclerosis or rheumatoid arthritis, a cr viral material associated with multiple sclerosis or rheumatoid or arthritis, a polypeptide exhibiting an inhibitory activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by from MSRV, and an antibody directed against the MSRV-1 virus obtained by completed immunogenic agent consisting of the antiganic polypeptide defined above. The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis, or for detecting in a biological sample, the presence of or exposure to a virus associated with multiple sclerosis or rheumatoid arthritis. The present constantely determined. Note: The SEQ ID numbers for the sequences as displayed in the main body of the patent do not match the SEQ ID numbers constant the sequence listing consequently those sequences mentioned in the main and analyse in pare intended to claim.
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GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCCACTGTGCTCCTGATCCAGGAGNN 1020 TGGGTTTGTCCTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTCCTTCCATGAC 1140 TCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGGGAAGTGG 1260 GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGT 1020 1021 ACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCC 1080 TGGGTTTGTCCTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTCTTCCATGNN 1140 CCACGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTA 1200 1141 ccacescrictaaradascraraacacrcacescaresccaasarrccarrcerresnn 1200 rerereaceceacaaceceacereacaaaancreacerreceacearricecaacrnn 1260 CCCACTGCCATTTTGGTAGCGGCCCACCACCATCTTGGGAGCTGTGGGGAGCAAGGATCCC 1320 960 CTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTTTGCCACCGTCACAGACCCGCN 960 720 780 780 840 840 900 661 ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCN 720 CACTCTATTTCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGG 900 601 ANCTGGGAAGGTGACCGCATCCATCTTAAACATGGGGCTTGCAACTTAGCTCACACCCN 660 Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; AATCATCTATTGCCTGAGAGCACAGCGGGAAGGACAAGGATTGGGATATAAAACTCAGGCN CACTCTATTTCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGN 1021 ACCCATIGCCACTCCCGATCAGGCTAAAGGCTTGCTTGTTCCTGCATGGCTAAGTGNN TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTN CTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGACCCGCT ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC AATCATCTATTGCCTGAGAGCACAGGGGAAGGACAAGGATTGGGATATAAACTCAGGCA TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT Colon adenocarcinoma related gene sequence SEQ ID NO:81. BP. ABL61744 standard; DNA; 56093 CCAGTAACA 1329 1321 CCAGTAACA 1329 (first WO200194629-A2. Homo sapiens 15-MAY-2002 13-DEC-2001 1321 721 901 1081 1081 1141 1201 1201 1261 ABL61744; gene; ds. 661 721 781 781 841 841 901 961

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18-SEP-2000; 2000US-0234139.
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20-SEP-2000; 2000US-0234094.
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Soppet DR, Weaver Z;
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8 X C C C g 셤 원 g g a 셤 셤 셤 셤 원 셤 g g g ò ò ò ò à ò ò à ò ò 8 8 ò ò ò à The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an arti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oseophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set. Horrigan Endress G, a, Ebner Claim 1; SEQ ID NO 81; 44pp; English Ϋ́

37545 37845 37197 37257 37317 37318 cGAAGCTGTAAAACTA------CAAATGGAGCCCAAGATGCAGTCCAAGACTAA 37365 37425 37485 37605 37665 37725 37726 AATCATCTATTGCCTGAGAGCACAGGAGGAGGACAATGATGGTCGGGATATAAACCCAAGTC 37785 37905 37077 37137 ď 120 360 420 540 900 096 180 240 009 099 780 840 cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's 300 480 720 9 61 AGGGGAAGAATGCTGTTAGTATGTTAATCTGGAATCATTACTGAGAAGGTTAAAGA 37078 AGGGAAGAATGCTGTTATTATGTTAATCAATCCGGAATCGTCACTGAGAAAGTTAAAGA 37258 GCTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTTTCCAGAAT 37366 GATCTACCGCAGACCCCTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAA AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG 37486 AAGCAGITAGAGCGGTCGTCGGCCAACCCCCAACAGCACTTAGGTTTTCCTGTTGAGA 37546 TGGGGGACTGAGAGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCT 37606 AGCTGGGAAGGTGACCACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACTG 37666 ACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAGACAGGAGGTAAAGAAATAGCC AATCATCTATTGCCTGAGAGCACAGCGCGGAAGGACAAGGATTGGGATATAAACTCAGGCA 17786 TICGAGCCGGCAACGCCAACCCCCTTTGGGCCCCCCTCCCTTTGTATGGGAGCTCTTTTTT CACTCTATTTCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGG CTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGACCCGCT 1 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTT 37018 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTATTTT 121 AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGCCT 37198 CCTCAGCCAATGGATGCCCTGGATTCTCCCCCTTCTAGGACCTCTAGCAGCTATAATATT 301 TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 361 AATCTACCGTGGACCCCTGGCTGCTAGACTATGCTCTGATGTTAATGACATTGA 481 AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT CCTCAGCCATGGATGCCCTGGACTCTCCCTTCTTAGGACCTCTAGCAGCTATAATATT 241 TTTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT 541 GGGTGGACTGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT 601 ANCTGGGAAGGTGACCGCATCCATCTTAAACATGGGGCTTGCAACTTAGCTCACACCCG 661 ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC Gaps Sequence 56093 BP; 16164 A; 12346 C; 10702 G; 16881 T; 0 U; 0 Other; DB 6; Length 56093; 13; 0; Mismatches 111; Indels Score 1035.2; Pred. No. Query Match 77.9%; Best Local Similarity 90.1%; Matches 1133; Conservative 181 421 721 781 901 841 tumour

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biological activity; genetic engineering; hybridisation probe; oligomer;
primer; chromosome mapping; gene mapping; recombinant protein production;
                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides, useful as hybridization probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA.
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                                                                                                                                             GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGT
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                                                                                                                                                                                                                                                    1 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTTTTT
                                                                                                                                    Query Match 77.5%; Score 1029.4; DB 10; Length 9502; Best Local Similarity 87.9%; Pred. No. 0; Matches 1178; Conservative 0; Mismatches 129; Indels 33;
                                                                                   0 U; 1 Other;
  sequence represents a human contig polynucleotide in an example from the present invention.
                                                                                   2263 T;
                                                                                   Sequence 9502 BP; 2813 A; 2433 C; 1992 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid sequences of human endogenous retrovirus, HERV-7g, usdiagnosis, treatment and prevention of autoimmune and neurological
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The peptides may also be used (by sequence comparison) to detect/ide endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence used to illustrate the invention
                                                                                                                                                Query Match 77.0%; Score 1023.2; DB 3; Length 10499; Best Local Similarity 90.1%; Pred. No. 0; Matches 1132; Conservative 0; Mismatches 111; Indels 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomeras, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed activity of (II) to useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The
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polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                        TAACAGAGCTATAACACTCACCGCATGGCCCAAGGTTCCGTTCCTTGTAATCCGTGAGGC 4389
                                                              CAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGGGAAGTGGCCCACTGCCA 1270
                                                                                                                                                TTTTGGTAGCGGCCCACCACCATCTTGGGAGCTGTGGGAGCAAGGATCCCCCAGTAACA 1329
                                                                                                                                                                        TCTTGGAAGTGGTTCACCACCATCTTGGGAGCTCTGTGAGCAAGGACCCCCCGGTAACA 4508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chalup MS, Chang SC;
C, Daniels SE, Dufour GE;
JL, Jones AL, Liu TF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, receptor, diagnostic, therapeutic, gene therapy, vaccine, cell proliferative disorder, Crohn's disease, lymphoma, leukaemia, acquired immune deficiency syndrome, AIDS; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spiro PA, Banville SC, Shah P, Chalup MS, Ch as SA, Amshey S, Dahl CR, Dam TC, Daniels SE, Pong WT, Greenawalt LB, Hillman JL, Jones AL,
                                                                                                                                                                                                                                                                                                                                                                                                                        Human diagnostic and therapeutic polynucleotide (DITHP) #17
                                                                                                                                                                                                                                                                                               AAS31002 standard; cDNA; 1393 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 FEB-2000; 2000US-0184697P.
24 FEB-2000; 2000US-0184697P.
24 FEB-2000; 2000US-0184697P.
24 FEB-2000; 2000US-0184769P.
24 FEB-2000; 2000US-0184771P.
24 FEB-2000; 2000US-0184771P.
24 FEB-2000; 2000US-0184773P.
24 FEB-2000; 2000US-0184774P.
24 FEB-2000; 2000US-0184777P.
24 FEB-2000; 2000US-0184777P.
24 FEB-2000; 2000US-0184877P.
24 FEB-2000; 2000US-0184871P.
24 FEB-2000; 2000US-018481P.
24 FEB-2000; 2000US-018481P.
24 FEB-2000; 2000US-018481P.
24 FEB-2000; 2000US-018481P.
24 FEB-2000; 2000US-018481P.
24 FEB-2000; 2000US-018481P.
26 FEB-2000; 2000US-0185218P.
15 MAY-2000; 2000US-0204825P.
16 MAY-2000; 2000US-0204821P.
16 MAY-2000; 2000US-0204821P.
16 MAY-2000; 2000US-0204821P.
17 MAY-2000; 2000US-0204821P.
17 MAY-2000; 2000US-0204821P.
17 MAY-2000; 2000US-0204821P.
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17-MAY-2000; 2000US-0205285P.
17-MAY-2000; 2000US-0205286P.
17-MAY-2000; 2000US-0205287P.
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Chen A, D'
Flores V,
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the invention relates to polymulation that include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and (II) porteins involved in growth and development and receptors. (I) and (II) and be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DITHP expression. For example, (I) and (II) expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPs, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder, or supplementing the patient's own production of them. (I) and (II) may be used to produce the DITHPs, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in camples, and therefore which patients may be in need of restorative captorative antibodies against DITHPs and in assays to identify modulators of DITHP captobes and activity. The anti-DITHP antibodies and anti-DITHP antibodies may also be used as diagnostic agents for detecting the arti-DITHP antibodies may also be used as diagnostic agents for detecting the anti-DITHP antibodies may also be used as diagnostic agents for detecting the greence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)), AASJOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSSE-ABSOSS
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                                                                                                                                                                                                                                                                                                                Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides (I) encoding diagnostic and
A;
W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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                                                    Chen .
             Daffo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
             Stockdreher TK, D.
DL, Bratcher SR,
Jackson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 778.8; DB 4;
Pred. No. 1.1e-244;
0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DITHP) polynucleotides of the invention
             Roseberry AM, Rosen BH, Russo FD,
Wright RJ, Yap PE, Yu JY, Bradley
Cohen HJ, Hodgson DM, Lincoln SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 304; 522pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.6%;
Best Local Similarity 87.2%;
Matches 904; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to
                                                                                                                                                                                         2001-502867/55.
                                                                                                                                                                                     WPI; 2001-502867/
P-PSDB; AAU19431.
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1320 CCTCAGCCAATGGATGCCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATT 1379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .440 rgaagcrgraaagcracagarggrcrracaaarggaaccccagarggagrccargacra.1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1200 AGGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGA
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92.8%;
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Matches 812; Conservative
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                                                                                    CCCAAGCATTCGAGCAACGCTGCCCCCTTTGTGTCCCCCCTTTGTATGGGAGC
                                                                                                                                                                                                                                                          590 TGTTACGGTTTGAGCTTTCGCTCGCCGTCCACCACCACCACGTGTTTGCCGCCATCGGA
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                                                                                                                                                                                                                                  TTTTATGGCTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACA
Nucleotide sequence of the MSRV-1 3' env and LTR regions.

    1629
    /*tag= a
    /note= "Contains one termination codon"

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Gaps

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Indels

Score 775.4; DB 3; Pred. No. 1.8e-243; 0; Mismatches 63;

Length 2030;

1259

1319

240

300

360

180

1559

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The present sequence represents the nucleotide sequence corresponding to the 3' env region and long terminal repeat sequences from clone CL6 of Multiple Sclerosis retrovirus (MSKV-1). The specification describes a long terminal repeat (LTR)-RUS region which encodes the expression of a MSRV-1 protein. This is unusual for LTRs, in particular in the RUS region. The sequence includes CAAT and TATA signals which are present in the UB and R regions and are not directed towards the CDS indicated in the features table. Probes and antibodies to the MSRV-1 retrovirus protein and encoding polymucleotide sequences are used to detect the presence of MSRV-1 retrovirus in a biological sample. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tide fragment of LTR-RUS region from Multiple Sclerosis retrovirus used to detect the presence of MSRV-1 retrovirus in a biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2030 BP; 574 A; 559 C; 387 G; 510 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                              Komurian-Pradel F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 23pp; English.
                                                                                                                                                                                                                                                                                                              Perron H,
                                                                                                 99EP-00420041
15-FEB-2000; 2000WO-IB000159
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and nucleic acid molecules encoding such proteins. EMBRY sequences are useful for screening modulators useful for treating or preventing disorders associated with abnormal expression of EMBRY. The disorders treated include reproductive disorders such as infertility. The disorders endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory disorder such as acquired immune deficiency syndrome (AIDS), allergies, context dermatitis; disorders of the placenta such as preclampsia, abruptio placentae etc. Sequences of the invention are also useful for analysing a proteome of a tissue or a cell type. EMBRY proteins are useful as immunogens for preparing antibodies. Polynucleotides of the invention are useful for creating knockin humanised animals or transgenic animals to model human diseases. They are also used in gene therapy. The present sequence is human EMBRY-2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1503 reaagcrigraaagcracaaarggrrcrrcaaarggagccccagargcagrccargacraa 1562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2074;
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modulators useful for treating or preventing disorders endometriosis, infertility, allergy, preeclampsia.
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Pred. No. 1.2e-240;
0; Mismatches 60;
                                                                               96-97; 97pp; English
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93.0%;
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Best Local Similarity 93.0
Matches 812; Conservative
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                                                                                                                                                                                                                                                                 1740 AGCTGGGAAGGTGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCCG
     AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGGTTTTCCTGTTGAGA
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/product= "EMBRY-2 protein"
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64. .1692
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124. .1689
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P-PSDB; AAE25054.
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                                                                                                                                                                                                                                                                                                                                                                                                                           connective tissue disorder; drug screening; proteome analysis;
gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
disease model; toxicological testing; transcript imaging; growth;
                                                                                                                                                                                                                                                                                                                                                                                              disorder;
                                                              TTCAAGCCAGCAACAGCCACTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                              disorder;
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Amshey SR;
d Y, Gerstin E
SR, Harris B;
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                                                                                                                                                                                                                                                                                                                                Human dithp growth/development-associated protein-encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                              cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic neurological disorder; gastrointestinal disorder; transport dis
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                                                                                                                                          CACTCTATTTCACTCTATTAAATCTTGCAACTG 2074
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29-MAR-2001; 2001US-0280067P.
29-MAY-2001; 2001US-0281068P.
17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
20-JUN-2001; 2001US-0299476P.
                                                                                                                                                                                                                                   ACC46747 standard; cDNA; 2046
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Daughtery SC, Dam TC,
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P-PSDB; ABR41810.
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Flores V,
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transgenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for DITHP proteins; microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein sequences; methods of screening for compounds which specifically bind a DITHP protein; and methods of sessessing the toxicity of test compounds using a dithp hybridiastion probe. Dithp nucleic acid sequences and DITHP proteins may be used in the diagnosis of a wide variety of conditions including cancer and other cell conditions of inflammatory disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; metabolic disorders; neurological disorders; gastrointestinal disorders; transport of sorders; and connective tissue disorders. They may also be used to screen for modulators of protein activity or gene expression. DITHP proteins can additionally be used in analysis of the proteome of a tissue additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of antisense sequences, as a source of continued and equal testing, and in transcript imaging the generation of transgenic animal models of human disease or knock in the present sequence represents a dithp cDNA encoding a DITHP protein continued in electronic format directly from MIPO at this patent did not form part of the printed specification, but was continued in electronic format directly from MIPO at
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                                                                                                                                                                                                                                            bone marrow, treatment; prevention; nutrition; cytokine; immune; vaccine; cell proliferation; cell differentiation; suppressor; tumour inhibition; haematopoiesis regulator; activin; inhibit; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.
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This invention describes novel human secreted proteins encoded by polynucleotides isolated from human adult testes, adult brain, adult blood or adult placenta, or murine adult bone marrow or thymus cDNA libraries. The products of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, haemacopoiesis regulating e.g. as vaccines) or suppressing activity, activity, activity, chemotactic/chemokinetic activity, chemotactic/chemokinetic activity, receptor/ligand activity, activity, activity, cacherin/tumour invasion suppressor activity, anti-inflammatory activity, cacherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for
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Pred. No. 5e-229;
0; Mismatches 69;
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Best Local Similarity 90.7%;
Matches 794; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the human secreted protein AJ172 2 nucleotide sequence, obtained from a human adult testes CDNA library. The invention relates to secreted human and mutrine proteins. The polymocleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Detection of the levels of the proteins can be used for the diagnosis of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested cativities include nutritional activity (e.g. in feeds), cytokine and call proliferation/differentiation activity, immune stimulating de.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, cactivity, acceptor/ligand activity, anti-inhammatory activity, cacherin/tumour inhabition activity. The
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             TICAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used to develop
                                                                                                                                                                                                                                     Human, secreted protein, disease diagnosis, pre-eclampsia, cancer, placental pathology, metastasis inhibition; nutritional activity; immune stimulator; haematopoiesis regulator; tissue growth; tumour inhibitor; anti-inflammatory; clone AJ172_2; ATCC_98115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides encoding secreted cDNA libraries, used to de products for the diagnosis and treatment of neoplastic disease.
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Pred. No. 5e-229;
0; Mismatches 69; Indels 12;
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                                                                                                                                                                                                             Human secreted protein AJ172_2 polynucleotide sequence
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                                                               CATGCTATTTCACTCTATTAAATCTTGCAACTGCA 2929
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                                              CACTCTATTTCACTCTATTAAATCATGCAACTGCA
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                                                                                                                                    AAZ59468 standard; cDNA; 2946
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Best Local Similarity 90.7%;
Matches 794; Conservative
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Merberg D, Mi S, Treacy M;
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TCAAAATCGAAGACTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTT
                        TCAAAATCGAAGGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTATTTTT
                                                                                         AGGGGAAGAATGCTGATATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA
                                                                                                                                                                                   AATTTGAGATCGAATATAATGTAGAGCAGAGCCTTCAAAACACTGCACCCTGGGGCCT
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useful as inhibitors of receptor/ligand interactions. The psequence represents cDNA encoding a human secreted protein.

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autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; allergic reaction; asthma; myeloid cell deficiency; lymphoid cell deficiency; osteoporosis; osteoarthritis; peripheral nervous system disease; peripheral neuropathy; Alzheimer's disease; Parkinson's disease; coagulation disorder; inflammatory disease; systemic inflammatory response syndrome; SIRS; ischaemia-reperfusion injury; Crohn's disease; anaphylaxis; hyperseenstituity; regeneration; neural cell proliferation; fertility; tumour; chemokine; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteins A23021 encoded by clone A23021 from human adult colon, and BD12716 encoded by clone BD12716 from human fetal kidney cDNA library, useful for treating e.g. multiple sclerosis and rheumatoid arthritis.
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Spaulding V, Carlin-Duckett M;
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Treacy M, Bowman MR,
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Kelleher K;
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02-JUN-1997
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The invention relates to a protein comprising fully defined AZ302 1

protein or BD127 1 6 protein. The polymucleotides are useful for

expressing recombinant proteins for analysis and are also useful as

chromosome markers or tags to identify chromosomes or to map related gene

chromosome markers or tags to identify chromosomes or to map related gene

continue. The proteins are useful as amino acid supplement, carbon

source, nitrogen source and carbohydrate source. The proteins are useful

corrections (erg. manned deficiencies and disorders (e.g. multiple

combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple

sclerosis, systemic lupus erythematosus, rheumatoid arthritis), allergic

cactions (e.g. asthma), myeloid or lymphoid call deficiencies,

cactions (e.g. asthma), myeloid or lymphoid system disease),

cosquise or osteoarthritis, peripheral nervous system disease),

cosquise syndrome (SIRS), ischaemia-reperfusion injury, Crohn's disease),

cappination disorders, inflammatory diseases (e.g. systemic inflammatory

responses syndrome (SIRS), ischaemia-reperfusion injury, Crohn's disease),

anaphylaxis and hypersenativity. Proteins are also useful for inducing

tumour immunity, for inducing bone, cartilage, tendon, ligament and/or

cregenerating nerve and brain tissue, for inducing fertility and for

inhibiting tumour growth. Proteins are also useful as chemokine for

mammalian cells (e.g., monocytes, fibroblasts, neutrophils), and also

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                                                                             55.1%; Score 731.8; DB 10; Length 2946; 90.7%; Pred. No. 5e-229;
                                                                                                                     12;
                                              Sequence 2946 BP; 858 A; 801 C; 570 G; 717 T; 0 U; 0 Other;
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Matches 794; Conservative
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                                                                                                                                                                                                                                                                          AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT
                                                                   TGAAGCTGTAAAAGCTACAAATAGTTCTTCAAATGGAACCCCCAGATGCAGTCCATGACTAA
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/product= "envelope protein"
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; cancer; cell adhesion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to identifying compounds which are modulators of syncytin expression. The syncytin modulators are useful in diagnosis and treatment of preeclampala and gestational trophoblast disorders (e.g. choriocarcinoma, hydatiform mole, placental site tumour and missed incomplete abortion). Syncytin is a human gene derived from the envelope gene of human endogenous defective retrovirus, HERV-W. The present invention is based partly on the discovery that syncytin expression is dramatically reduced in preeclampsia, and is also mis-localised to the apical syncytiotrophoblast membrane. The present sequence is human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a compound for treating a subject with or at risk of developing preeclampsia, comprises determining whether the expression or activity of syncytin in the cell is modulated in the presence of a test compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTCAGCCAATGGATGCCCTGGACTCTCCTTCTTAGGACCTCTAGCAGCTATAATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                               Human; syncytin; preeclampsia; gestational trophoblast disorder; choriocarcinoma; hydatiform mole; placental site tumour; abortion; envelope gene; human endogenous defective retrovirus; HERV-W; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 39-42; 43pp; English
                                                                                                                                                                                                                                                                      /product= "Syncytin"
                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             07-JUL-2000; 2000US-0216657P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-171727/22
                                                                                   Human syncytin cDNA
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The invention relates to isolated polymucleotide (I) and polypeptide (II)

sequences. (I) is useful as hybridisation probes, polymerase chain

reaction (PCR) Primers, oligomers, and for thromesome and gene mapping,

and in recombinant production of (II). The polymucleotides are also used

in diagnostics as expressed sequence tags for identifying expressed

cons. (I) is useful in gene therapy techniques to restore normal

activity of (II) or to treat disease states involving (II). (II) is

useful for generating antibodies against it, detecting or quantitating a

polypeptide in tissue, as molecular weight markers and as a food

supplement. (II) and its binding partners are useful in medical imaging

of sites expressing (II). (I) and (II) are useful for treating disorders

involving abbrrant protein expression or biological activity. The

polypeptide and polynucleotide sequences have applications in

diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits to assess biodiversity
2609 AATCATCTATTGCCTGAGAGCACAGCAGGAGACAATGATCGGGATATAAACCCAAGTC 2668
                                                                                                                                                                                                                                                          721 AATCATCTATTGCCTGAGAGCACAGGGGAAGGACAAGGATTGGGATATAAACTCAGGCA
                                                            ACCAATCAGAGGGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC
                                                                                                                                                                                                                      TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #20014.
                                                                                                                                                                                                                                                                                                                                  2729 CAIGCIAITICACICIALIAAAICIIGCAACIGCA 2763
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                                                                                                                                                                                                                                                                                            protein. The specification describes a method for detecting expression of an envelope protein from a human endogenous retrovirus (HERV), in cells, of a tissue or culture. The method comprises detecting syncytia formation due to the fusogenic properties of the envelope protein. Envelope polypeptides and polymorleotides are used to produce therapeutic or prophylactic compositions, particularly for treatment of cancer, to correct defects in placental development (or other natural formation of other types of syncytia), and to promote adhesion of cells in grafts or cellular repair processes. Expression of sequences antisense to the polynucleotide are used to prevent formation of syncytia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCAGCCAATGCATGCCCTGGATTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT 2140
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                                                                                                                                                                              Detecting expression of human endogenous retrovirus envelope protein in cells of a tissue or culture, from its ability to induce syncytia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2141 GCTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTTGTCTCTTCCAGAAT
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                                                                                                                                                                                                                                                                              present sequence encodes a human endogenous retrovirus envelope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2781 BP; 747 A; 770 C; 556 G; 708 T; 0 U; 0 Other;
                                                                                    Bouton O,
                                                                                  Blond J, Lavillette D,
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0; Mismatches
                        BIO MERIEUX.
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                                                                                  Cosset F,
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and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 9.1e-228;
0; Mismatches 223;
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Best Local Similarity 78.6%;
Matches 1094; Conservative
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                   retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin- dependent diabetes and related pathologies) and of abnormal or susuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes associated with this susceptibility
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                                                                                                                                                                                                                                                            54.4%; Score 722.6; DB 2; 88.5%; Pred. No. 9.4e-226; iive 19; Mismatches 70;
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The present sequence represents an endogenetic retrovirus, which is associated with an autoimmune disease, and is integrated into the human genome. The retrovirus is human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. HERV-W nucleic acid fragments, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid from human endogenous retrovirus, useful e.g. for diagnosis of autoimmune disease and complications of pregnancy, contains at least part of the gag gene.
                                                                                                                                          Autoimmune disease; retrovirus; human endogenous retrovirus W; gag gene; pregnancy; multiple sclerosis; T cell proliferation;
7548 CATGCTATTTCACTCTATTAAATCTTGCARCTGCR 7582
                                                                                                                     Human endogenous retrovirus W (HERV-W) sequence.
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AAX25660 standard; cDNA to mRNA; 1136

RESULT 21
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This sequence represents clone cl.C4C5 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulindependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes
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                                                                                           Clone, human endogenous retrovirus, genome, autoimmune disease, multiple sclerosis, rheumatoid polyarthritis, insulin-dependent diabetes, disseminated lupus erythematosus, pregnancy, chromosomal marker, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
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Pred. No. 8.7e-226;
0; Mismatches 75;
                                                 Human endogenous retrovirus W clone cl.C4C5
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                                                                                                                                                                                                   Human endogenous retrovirus
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(first entry)
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tes 787; Conserv
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integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell proliferation in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATCATCTATTGCATGAGAGCACAGGAGGACAATGATCGGGATATAAACCCAAGTC 1021
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                                                                                                                                                                      Length 1136;
                                                                                                                                              Sequence 1136 BP; 336 A; 289 C; 241 G; 270 T; 0 U; 0 Other;
                                                                                                                                                                                                  Indels
                                                                                                                                                                      54.3%; Score 721.2; DB 3;
90.0%; Pred. No. 8.7e-226;
iive 0; Mismatches 75;
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nes 787; Conservative
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fragment, which is associated with an autoimmune disease, and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HERV-W;
                                                                   AGGCACCCTCCTGAGGAAATCTCAGCTGCACAACCTCTACTACTACGCCCCAATTCAGCAGG
                                                                                                                                                                                                                                                                                           ACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAGACAGGAGAGATAAAGAAATAGCC
                     GATCTACCGCAGACCCCTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAA
                                                                                                    AAGCAGTTAGAGCAGTTGTCAGCCAACCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
                                                                                                                                AAGCAGTTAGAGCGGTCGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
                                                                                                                                                           GGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
                                                                                                                                                                                     regeggacreagacacaccraecregarriccraegcreacraagaarcccraagccr
                                                                                                                                                                                                                  ANCTIGGGAAGGTGACCGCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCG
                                                                                                                                                                                                                                          Agcriegeaagereaccacarccaccrrraaacaceeeerrecaacrracaaccre
                                                                                                                                                                                                                                                                        ACCAATCAGAGGTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC
                                                                                                                                                                                                                                                                                                                              AATCATCTATTGCCTGAGAGCACAGCGGAAGGACAAGGATTGGGGATATAAACTCAGGCA
                                                                                                                                                                                                                                                                                                                                                                                    TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT
                                               AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and 3' non coding sequences of HERV-W from human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid from human endogenous retrovirus, useful e.g. for diagnosis of autoimmune disease and complications of pregnancy, con at least part of the gag gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Autoimmune disease; retrovirus; human endogenous retrovirus W; gag gene; pregnancy; multiple sclerosis; T cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATGCTATTTCACTCTATTAAATCTTGCAGCTGC 1115
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                                                                    2202 cgaagcrigrgaacra------caariggagcccaagargcagrccaagacraa 2249
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                                    TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
                                                                                                         AATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGATGACATTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents clone cl.PH74 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulindependent diabetes and related pathologies) and of abnormal or susceptiblity to these conditions, or proximity markers for associated with this susceptibility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
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                                                                                                                                                                                                                                                 Clone; human endogenous retrovirus; genome; autoimmune disease; multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes; disseminated lupus erythematosus; pregnancy; chromosomal marker; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 712.6; DB 2; Length 2
Pred. No. 1e-222;
0; Mismatches 81; Indels
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Mandrand B,
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Best Local Similarity
Matches 782; Conserv
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                                                                                   fragment, which is associated with an autoimmune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W HERRV-W). The HERRV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell
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disease and complications of pregnancy, contains
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                                                                                                                                                                                                                                                                                                                                                Score 712.6; DB 3; Length 2782;
Pred. No. 1e-222;
0; Mismatches 81; Indels 12;
                                                                                                                                                                                                                                                                                                              Sequence 2782 BP; 741 A; 767 C; 565 G; 709 T; 0 U; 0 Other;
                                                    Disclosure; Page 46-47; 53pp; French
                  least part of the gag.gene
                                                                                                                                                                                                                                                                                                                                                  53.6%;
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Best Local Similarity 89.4
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endogenous retrovirus (HERVs) the full length endogenous provirus which
                                                                                    TTCGAGCCCGCCAACGGCAACCCCCTTTGGGTCCCCTTTGTATGGGAGCTCTGTTTT
2610 AATCATTTATTGCCTGAGAGCACAGCAGGAGGACAATGATCGGGATATAAACCCAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein; envelope protein; multiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective; antisense-therapy; autoimmune disorder; ds.
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designated HERV-W. The present invention describes proteins or peptides (1) having superantigne (SAG) activity comprising the ENV protein (ENV) of HERV-W, the surface protein (SU) and transmembrane (TM) sub-units. (I) have neuroprotective activity, and can be used in: vaccines, antisensetherapped, and HERV-W SAG activity-inhibitors. (I) and encoding DNA/RNA are useful for diagnosing multiple sclerosis (MS) or HERV-W-associated disorders. (I) are also useful for identifying substances (and optionally cerovering) capable of binding to a retroviral superantigen associated with MS, substances capable of blocking transcription or translation of HERV-W retroviral superantigen. A protein or peptide derived from (I), modified to be devoid of SAG activity and being capable of generating an immune response against HERV-W retroviral SAG is useful in therapy. Nucleic acid activity and being capable of blocking transcription or capable of blocking SAG activity, capable of blocking transcription or expected sencenting (I) are useful as vaccines against MS. Substances capable of blocking SAG activity, capable of blocking transcription or prevention of HERV-W retroviral superantigen for use in translation or prevention of MS. (I) and nucleic acid becoding (I) are useful for the treatment and prevention of MS. (I) and nucleic acid senceding them are useful for diagnosing autoimmune disease. The present sequence encodes the
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(SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                           Probe #4541 for gene expression analysis in human cervical cell sample.
                                                                                                                                   AATCATCTATTGCCTGAGAGCACAGCGGGAAGGACAAGGATTGGGATATAAACTCAGGCA
                                                                                                                   TTCAAGCCAGCAACAGCAACCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTTTTT
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Pred. No. 3e-220;
0; Mismatches 79; Indels 9;
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPD
                                                                                                                                                                                              nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 4642; 639pp + Sequence Listing; English
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DR;
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GTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTTTCCAGAAT
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producing a microarray for predicting, measuring and displaying ge expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders
                                                                                                                                                       6
                                                                                                           Score 704.8; DB 4; Length 1894;
Pred. No. 3e-220;
0; Mismatches 79; Indels 9;
                                                                           Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
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AGGCACCCCTCCCGAGGAAATCTCAACTGCACAACCTCTACTACGCCCCAATTCAGCAGG
                                                                                                                                     GGGGGGACTGAGAACAGGAATAACTAGATTTCCTAGACCAACTAAGAATCCCTAAGACT
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0668408
03-AUG-2000; 2000US-0224687P.
27-SEP-2000; 2000US-0224687P.
04-OCT-2000; 2000GB-00024263.
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                                                                                CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATATATT
Probe #4444 for gene expression analysis in human heart cell sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the from human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of freqions of genomic DNA predicted to encode protein. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from ganners esquence is a single exon nucleic acid probe of the invention. Note: The present sequence is a single exon nucleic acid probe of the printed specification, but was obtained in the print of the printed sequence data for this in the present sequence data for this in this factor of the printed specification, but was obtained the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAGTTAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4517; 327pp + Sequence Listing; English.
                                                                                                                                                                Human breast cell single exon nucleic acid probe #4517
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000GB-00024263.
          ABA45822 standard; DNA; 1894
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000662
                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-496933/54.
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                                                                                                                01-FEB-2002
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                                                                                                                                                                                                                                                      cancer; 88.
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                                                                                                                                                                        661 ACCAATC-----AGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAA
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                 GGGTGGACTGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
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                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease, Nopertension, cardiac arrhythmias and for form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                         NO 4444; 530pp; English
                                                                                                                                                                                     Rank
                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                     Chen W,
               2000US-0180312P.
2000US-0207456P.
2000US-00608408.
                                                             03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023659.
04-0CT-2000; 2000GB-00024269.
                                                                                                                                                                                     Penn SG, Hanzel DK,
                                                                                                                                                                                                                      WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID
              04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
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completed: January 22, 2005, 16:40:42
he: 618.913 secs
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TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTT

Gaps 6

Score 704.8; DB 4; Length 1894; Pred. No. 3e-220; 0; Mismatches 79; Indels 9;

53.0%; 89.7%;

Best Local Similarity 89.7 Matches 770; Conservative

Query Match

61 AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA 120

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GITACTCCICITIGGACCCIGIATCITIAACCICCITGITAAGTITGICITITCCAGAAT 1260

TGAAGCTGTAAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA

TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT

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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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(cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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TUKE, PHILIP
INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL.
THERAPEUTIC PURPOSES
                                                                      12, Appl
14, Appl
11, Appli
3, Appli
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3670, A
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COMPUTER READBELE FOLL.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETCATION DATA:
RAPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-NO. 6582703-1997
CLASS! FILOATION: UNMERR: US/08/979,847B
FILING DATE: 26-NO. 6582703-1997
ATTORNEY/AGENT INFORMATION:
NAME: BERRIOGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 300.024
REFERENCE/DOCKET NUMBER: 39046A
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-2787
; INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 1329 base pairs
TYPE: nucleic acid
                                                                                                              US-08-766-528-1
US-09-661-888-1
US-09-661-888-3
US-09-61-898-3
US-09-513-999C-26710
US-08-258-420-9
US-08-258-420-9
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US-09-513-999C-13878
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US-09-232-278A-5
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID
US-08-979-847B-108
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ADDRESSEE: OLIFF & BERRI
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
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GARSON, JEREMY
TUKE, PHILIP
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1021 ACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCTCCTGCATGGTTCCTGCATGGCTAAGTGCC 1080 1021 ACCCATTGCCACCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCC 1080 081 TGGGTTTGTCCTAATAGAACTGAACACTGGTTCCATGGTTCCTTCC	Application US/09175928A Application US/09175928A 3312921 38M4ZION: Jacobs, Kenneth McCoy, John M. Lavallie, Edward R. Collins-Racie, Lisa A. Evans, Cheryl Merberg, David Treacy, Maurice Mi, Sha Genetics Institute, Inc. WINTION: SERETED PROTEINS AND POLYNUCLEOTIDES ENCE: 6006B.AJ172A PLICATION NUMBER: US/09/175,928A FLING DATE: 1998-10-20 PAGE HOMO Sapiens Homo sapiens	Query Match 55.1%; Score 731.8; DB 3; Length 2946; Best Local Similarity 90.7%; Pred. No. 7.7e-240; Matches 794; Conservative 0; Mismatches 69; Indels 12; Gaps 1; Qy 1 TGAAAATCGAAGAGTTTAGACTTGCTAACCGCCAAAGAGGGGGAACCTGTTTATTTT 2126 Db 2067 TCAAAATCGAAGAGTTTAGTTATTATCAATCGACTGAAGAGGGGGAACCTGTTTATTTT 2126 Oy 61 AGGGGAAGAATGCTGTTAATTATGTTAATCAATCGGAATCATCGAGAAAGTTAAAGA 120 Db 2127 AGGGGAAGAATGCTGATAATTATGTTAATCAATCCGGAATCGTCACTGGAAAGATGAACACTGGAAGAGTTAAAGA 2186 Oy 121 AATTCGGAATCGAATAATAATCAAGAGGAGAGAGAACACTGGAACCTGGGGCCT 180 Db 2187 AATTCGGAATCGAAAACACGAGAGAGAGAGAGACTTCGAAACACTGGACCTGGGGCCT 2246 Oy 181 CCTCAGCCAATGGAACCCTGGAATCCTCCCCTTCTTAAGGACCTCTAGGAGCTTAAAATATT 2306 Oy 2247 CCTCAGCCAATGGAACCCTGGAATCCTCCCCTTCTTAAGGACCTCTAAGAATATT 2306 Oy 2247 CCTCAGCCAATGGAACCCTGGAATCCTCCCTTCTTAAGGACCTCTAAGACATAAAATTT 2306 Oy 2241 TTTACTCCTCTTTGGAACTCCTCTTATAAGATTTTTTTTT
Query Match 99.8%; Score 1326; DB 4; Length 1329; Best Local Similarity 100.0%; Pred. No. 0; 0; Indels 0; Gaps 0; QV 1 TCAAATCGAAGAGTTTAGATTGCTAACCGCCAAAGAGGGGGAACCTGTTTATTTTT 6 Indels 0; Gaps 0; O; QV 61 AGGGAAGAATGTTAGATTGTTAACCAACGGCGAAAGAGGGGGAACCTGTTATTTTT 6 D D Db 61 AGGGAACAATGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA 120 D D Db 61 AGGGAACAATGCTTAGTAATGTTAATGTTAATCTGGAATCATTACTGAGAAGTTAAAGA 120 D D QV 121 AATTTGAGATCGAATATAATGTTAGGAGCAGAGGACCTTCAAAACACTGCACCTGGGGCCT 180 D Db 121 AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCTGGGGCCT 180 QV 181 CCTCAGCCAATGGATGCTGGACTCTCCCCTTCTTAGGAACTTAATATTT 240 QV 181 CCTCAGCCAATGGATGCCTGGACTCCCCTTCTTAGGAACTTTAAGCTATACTTATAATTT 240 QV 241 TTTACTCCTTTTGGACCCTGGAACTTCTTAAGCTTTCTTCCAGAAT 300 Db 241 TTTACTCCTTTTGGACCCTGTAATCTTCTAAACTTTCTTT	301 TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 301 TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 301 TGAAGCTGTAACGGACCGGCCTGCTAGAACCCCCAGATGCAGTCCATGA 301 AATCTAACCGTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA 421 AATCTAACCGTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA 421 AATCTAACCGTGGAAATCTCAACTGCACACACTCTAGTGTGG 421 AATCTAACCGTCGGAAATCTCAACTGCACAACCCCTACTACACTTCAGTAGG 481 AAGCAGTTAGAGGAAATCTCAACTGCACAAGTACTTGGGTTTTAATGACATTCAGTAGG 481 AAGCAGTTAGAGGAAATCTCAACTGCAACAGTACTTGGGTTTTCCTGTTGAGA 541 GGGTGGACTGAGAACCGCCAACAGTACTTGGGTTTTCCTGTTGAGA 541 GGGTGGACTGAGAACAGGCAACAGTACTTAAAAATTCCCAAATCCCAAAGCCT 601 AACTGGGAAGACACGCAACAGTACTAAGAATCCCAAAGCCT 601 AACTGGGAAGGTGACCAACTTAAAAATCCCAACAGCCCCG 601 AACTGGGAAGGTGACCCATCTTAAAACATGGGGCTTAAGCTCACACCCG 601 AACTGGGAAGGTGACCCATCTTTAAACATGGGGCTTAAGCTCACACACCCCG 601 AACTGGGAAGGTGACCCATCTTTAAACATGGGGCTTAAGCTCACACCCCG 61 AACTGGGAAGGTGACCCATCTTTAAAACATGGGGCTTAAGCTCACACCCCG 61 AACTGGGAAGGTGACCCATCTTTAAAACATGGGGCTTAAGCTCACACACCCCG 61 AACTGGGAAGGTGACCCATCTTTAAAACATGGGGCTTAAGCTCACACCCCG 61 AACTGGGAAGGTGACCCATCTTTAAAACATGGGGCTTAAGCTCACACACCCCG 661 AACTGGGAAGGTGACCCATCTTTAAAAAAAAACAGGAAACCCACCC	TAGAGAGCTCACTAAAATGCTAAT TATTGCCTGAGAGCACAGCGGGA TATTGCCTGAGAGCACAGCGGGA TATTGCCTGAGAGCACAGCGGGA TATTGCTACTGTACTTTGGC TTTCACTCTATTAAATCATGCAA TTTCACTCTATTAAATCATGCAA TTTCACTCTATTAAATCATGCAA TTTCACTCTATTAAATCATGCAA TTTCACTCTATTAGTTCGCCATCCACCTTTGGAA TTTCACTCTATTAGTTCGCCATCCACCTTTGAGTTCTTTGTTCGCCATCCACCTTTGTTTCGCCATCCACCTTTGTTTTGTTTCGCCATCCACCTTTGTTTTTTTT

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                                                                                      TELECOMPUTION:
REGISTRATION NUMBER: 30,024
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMPUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-6787
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
              APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSICTATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-979-847B-102
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US-09-513-999C-21394
; Sequence 21394, Application US/09513999C
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                                                                                                                                                                                                                                                       LENGTH: 635 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 92.4%;
Matches 572; Conservative
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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GCTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTTGTCTCTTCCAGAAT
                                                           AATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGATGACATTGA
                                                                                                                                          2595 TGGGGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCT
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                                       TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    841 CACTCTATTTCACTCTATTAAATCATGCAACTGCA 875
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PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 102, Application US/08979847B
Patent No. 6582703
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
BESEME, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOLIVET-REYNAUD, (
MANDRAND, BERNARD
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ADDRESSEE: OLIFF & BERI
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
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US-08-979-847B-102
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TUKE, PHILIP
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRACMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1199
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                                                                                                                                                                                                                                                                      COMPUTER READABLE FOLL...

COMPUTER READABLE FLORY disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PFLICATION NUMBER: US/08/979,847B
FILING DATE: 26-NO. 6582703-1997
CLASS: FICATION NUMBER: US/08/979,847B
FILING DATE: 26-NO. 6582703-1997
CLASS: FICATION NUMBER: WPB 39046A
ATTORNEY/AGENT INFORMATION:
NAME: BERRIOGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELEPHONE: 703-836-2787
; INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 base pairs
TVPE: nucleic acid
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                                                                                                                                 CORRESPONDENCE ADDRESS:
RADDRESSERS: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-08-979-847B-105
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GARSON,
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US-08-979-847B-127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCGTGTTTTTTATGGCTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1005 CCTGATCCAGCGAGGTACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCATGGCTAAGTGCCTGGGTTTGTCCTAATAGAACTGAACACTGGTCACTGGGTTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTCTCTTCCATGACCCACGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  766 ATATAAACTCAGGCATTCAAGCCAGCAACAGCA-ACCCCCTTTGGGTCCCCTCCCATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATAAAACCCAGGCATTCGAGCTGGCAACAGCAGCAGCCCCCTTTGGTTCCCTTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CCACCGCAGACCTGCCGCTGACTCCCATCCCTCTGGATCCTGCAGGGTGTCCGCTGTGCT
                                                                            TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PATECRA NO. 6/83361

PRICE REFERENCE: 59.052.REG
CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE PATENT. PM

SEQ ID NO 21994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 344.6; DB 4;
Pred. No. 1.3e-107;
1; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 105, Application US/08979847B
Patent No. 6582703
GENERAL INFORMATION:
BESINE, FREDERIC
PARANHOS-BACCALA, GLAUCIA
PAULICANT:
PRANTHOS-BACCALA, GLAUCIA
COMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1185 ATTCCATTCCTTGGTATCTGTGA 1207
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                     GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.9%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: k=g or t
US-09-513-999C-21394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 88.9
Matches 394; Conservative
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 102
                                                                     Duclert, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-08-979-847B-105
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLECTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
THERAPEUTIC PURPOSES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 CTGCATGGTCCAAGATTCCTTGGAATCCGTGAGACCCAGGACCAGGTCAGAGA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGTCCGCTGTGCTCCTGATCCAGCACAGGCGCCCATTGCCTCTCCCAATTGGGCTAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1051 CTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAATAGAACTGAACACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 crificcarretricriciacacactraacrecricecricaricaratreaceacreaciae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1111 TCACTGGGTTCCATGGTTCTCTTCCATGACCCACGGCTTCTAATAGAGCTATAACACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TCACTGGGTTCCACGGTTCTCTTCCATGACCCATGGCTTCTAATAGAGCTATAACACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1171 CCGCATGGCCCAAGATTCCATTCCTTGGTATCTGTGAGGCCAAGAACCCCAGGTCAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.4%; Score 257.8; DB 488.2%; Pred. No. 1.1e-77; ive 0; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BERRIDGE, PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-08-979-847B-126
                                                                                                                                                                                                                       PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       Sequence 126, Application US/08979847B
; Patent No. 6582703
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                         MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERF
STREET: P.O. BOX 19928
                                                                                                                                                       APPLICANT: PERRON, HERVE
BESEME, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 764 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                       JOLIVET-REYNAUD,
                                                                                                                                                                                                       BEDIN, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 126: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22320
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.2
Matches 291; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                    JS-08-979-847B-126
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                                                                                                                                                                                           INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRACMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANGTGAGGCTTGCCACCATTTGGGAAGTGGCCCACTGCCATTTTGGTAGCGGCCCACCAC 1290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCACTGGGTTCCATGGTTCTTCCATGACCCACGGCTTCTAATAGAGCTATAACACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTCCACTGTGCTCCTGATCCAGC-GAGGTACCCATTGCCACTCCCGATCAGGCTAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGTCCGCTGTGCTCCTGATCCAGCACAGGCGCCCATTGCCTCTCCCAATTGGGCTAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAATAGAACTGAACACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 265.2; DB 4; Length Pred. No. 3.3e-80; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1291 CATCTTGGGAGCTGTGGGAGCAAGGATCCCCCCAGTAACA 1329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO: 127:
                                                                                    KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                              MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
                                                             PARANHOS-BACCALA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 703-836-6400
                         FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                    BESEME, FREDERIC
BEDIN, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 210
PERRON, HERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                   ZIF: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.2
Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-979-847B-127
                                                                                                                                                                                                TITLE OF
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61 NTCANTARARICATNATINGGCARARACAGGAGGTARAGGARATAGCCARICATCTATIGC 120
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181 GGGCAACCCCTTTGGGTCCCCTCCCTTGTATGGGGGCTNTGTTTTCATGCTATTTCAN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOY, John
APPLICANT: LaVallie, Edward
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Reacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: BECREFED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
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APPLICATION NUMBER: US/08/721,489
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                     854 TCTATTAAATCATGCAACTGCA 875
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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Best Local Similarity 85.1
Matches 223; Conservative
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COUNTRY: U.S.A.
ZIP: 02140
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MOLECULE TYPE:
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                  .231 ANGTGAGGCTTGCCACCATTTGGGAAGTGGCCCACTGCCATTTTGGTAGCGGCCCACCAC 1290
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                                                            241 ACACAAGGCTTGCCACCATGTTGGAAGCAGCCCACCACTTTTGGAAGCAGCCGCGC 300
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CORRESPONDENCE ADDRESS: ADDRESSE: Genetics Institute, Inc. STREET: 87 Cambridge-Park Drive
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
                                                                                                                                                                  1291 CATCTTGGGAGCTGTGGGAGCAAGGATCCC 1320
                                                                                                                                                                                                                   301 TATCTTGGGAGCTCTGGGAGCAAGGACCCC 330
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5708157
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CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Matches 223; Conservative
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APPLICANT: Jacobs,
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Pred. No. 5.9e-46;
0; Mismatches 200; Indels
                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563C
FLING DATE: 02-AUG-1996
ATTORNEY/AGRNT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REGISTRATION NUMBER: 30,024
REGISTRATION NUMBER: 30,024
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 703-836-6400
700 South Washington Street, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 60.5%;
Matches 333; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                      COMPUTER READABLE FORM
                 Alexandria
                                           Virginia
: U.S.A.
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                                                                              22314
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TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCHEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: THERAPEUTIC PURPOSES
TUMBER OF SEQUENCES: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAGAGACAGGACTAGCTGGATTTCCTAGGCCGACTAAGAATCCCTAAGCCTAGCTGGG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAATCATCTATTGCCTGAGAGCACAGCGGGAAGGACAAGGATTGGGATATAAACTCAGG 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Indels
                                                                                                                                                          Sequence 3366, Application US/09621976
Fatent No. 6639063
GENERAL INPORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TILLE REFERENCE: GENSET, 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Frederic BEDIN
Glaucia PARANHOS-BACCALA
Florence KOMURIAN-PRADEL
Colette JOLIVET
Bernard MANDRAND
                                                  241 TNTATTAAATNTTGCAACTGCA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 58, Application US/08691563C Patent No. 6001987 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oliff & Berridge
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APPLICANT: Frederic BESEM
APPLICANT: Glaucia PARANH
APPLICANT: Glaucia PARANH
APPLICANT: Florence KOMUR
APPLICANT: COLETTE OJOLIVE
APPLICANT: Bernard MANDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 262; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                         RESULT 10
US-09-621-976-9366/c
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ADDRESSEE: C
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US-08-691-563C-58
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INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                               951 GATTĆCĊCTĊTGGAAGACACTACAACTGCAGGGCCCCCTTCTTGCCCCCTATCCAGCAGGA 1010
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781 ITACICACCTITGGGCCCTGIATITITAAGCTICTTGICAAAITIGTITCCTCTAGGAIC 840
                                                                                                                                                                                        -----AGCCTAGA 950
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                                                                              482 AGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGAG
                                                 GAAGCTGTAAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAAA
                                                                                                                                            362 ATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGAA
                                                                                                                                                                                                                                  422 GTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: BERRINGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
                                                                                                                                                                     901 TICTACCAAGGACCCCTGGAACGAICCACTGGCACTTCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 54, Application US/08979847B
Patent No. 6582703
GENERAL INFORMATION:
BESEME, FREDERIC
BEDIN, FREDERIC
BEDIN, FREDERIC
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MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-08-979-8478-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
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ADDRESSEE: OLIFF & BERE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleotide
STRANDEDNESS: single
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TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            667 TTACAGGAAAGGGCTTCTGATATCAGACAATGCCTTTCAAACTCTTATACCAA----C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 166; DB 4; Length 172
Pred. No. 5.9e-46;
0; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                                                                                                                ANDKESSEE: Oliff & Berridge STREET: 700 South Washington Street, Suite 300 CITY: Alexandria STREE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563
FILING DATE: 02-AUG-196
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFINCE/DOCKET NUMBER: WPB 38588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                        Glaucia PARANHOS-BACCALA
Florence KOMURIAN-PRADEL
Colette JOLIVET
Bernard MANDRAND
                                                                            Sequence 58, Application US/09374766; Patent No. 6579526; GENERAL INFORMATION: APPLICANT: Ferderic BESEME APPLICANT: Frederic BESIN APPLICANT: Frederic BEDIN APPLICANT: Frederic BEDIN APPLICANT: Florence KOWURIAN-PRADEI APPLICANT: Colette JOLIVET APPLICANT: Bernard MANDRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 60.5%;
Matches 333; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1722 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: 01iff & Be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-374-766-58
                                       RESULT 12
US-09-374-766-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 165; DB 3; Length 18 Pred. No. 1.4e-45; 0; Mismatches 247; Indels
PatentIn Release #1.0, Version #1.30
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                                       APPLICATION NUMBER: US/08/691,563C FILING DATE: 02-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                           NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38
TELECOWNUNICATION INFORMATION:
TELEPHONE: 703-836-6400
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46, Application US/09374766
Patent No. 6579526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.3%;
Matches 369; Conservative
                                                                                                                                                                                                                                                                                                     1859 base pairs
                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                       LENGTH: 1859 base pai
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: CDNA
US-08-691-563C-46
                                                                                                                                                                                                                                                                                                                                                                            linear
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SOFTWARE:
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Frederic BEDIN
Glaucia PARANHOS-BACCALA
Glaucia PARANHOS-BACCALA
Florence KOMURIAN-PRADEL
Colette JOLIVET
Bernard MANDRAND
WONTION: VIREAL MATERIAL AND NUCLEOTIDE FRAGMENTS
VENTION: VIREAL MATERIAL MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
VENTION: THERAPEUTIC PURPOSES
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                                                                    Gaps
                                                                    17;
                 Score 166; DB 4; Length 1722;
Pred. No. 5.9e-46;
0; Mismatches 200; Indels 1
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700 South Washington Street, Suite 300
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 46, Application US/08691563C; Patent No. 6001987
                 12.5%;
60.5%;
                   Query Match 12.5
Best Local Similarity 60.5
Matches 333; Conservative
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APPLICANT: Frederic BEDS
APPLICANT: Glaucia PARAL
APPLICANT: Glaucia PARAL
APPLICANT: Glaucia PARAL
APPLICANT: Glaucia PARAL
APPLICANT: Bernard MANDI
TITLE OF INVENTION: VIRI
TITLE OF INVENTION: THE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
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APPLICANT: Herve PERRON
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MEDIUM TYPE: Floppy
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STATE: Virginia
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US-08-691-563C-46
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLECTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA.
THERAPEUTIC PURPOSES
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                                            1551 Trotractgaggaccctragaccaaccccrggcccrtrcactggcctraaggggtt----
362 ATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGATGACATTGAA
                                                                                              422 GTCACCCTCCCGAGGAAATCTCCAACTGCACGCCCTACTACACTCCAATTCAGTAGGA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979, 847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1780 TGTGTCTAGCTAAAGGATTGTAAATGCAACAAT 1812
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NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PERRON, HERVE
BESENE, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-FRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BERRIDGE, PLC
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-979-8478-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-979-847B-42; Sequence 42, Application US/08979847B; Patent No. 6582703; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STREET: P.O. BOX 19928
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INFORMATION FOR SEQ ID NO: 42:
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TUKE, PHILIP
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STRANDEDNESS: single
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LENGTH: 1859 base pa
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                                                                                                                                                             VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
THERAPEUTIC PURPOSES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ATTTGAGATCGAATATAATGTAGAGCAGGACCTTCAAAACACTGCACCCTGGGGGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/374,766 FILING DATE:
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                   Glaucia PARANHOS-BACCALA
Florence KOMURIAN-PRADEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
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TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS: LENGTH: 1859 base pairs
                                                                                                                                                             Bernard MANDRAND
                                    Frederic BESEME
Frederic BEDIN
                                                                                                                                     Colette JOLIVET
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Matches 369; Conservative
                            APPLICANT: Frederic BESS
APPLICANT: Frederic BESS
APPLICANT: Glaucia PARAN
APPLICANT: Glaucia PARAN
APPLICANT: Clette JOLIV
APPLICANT: Bernard MANDR
TITLE OF INVENTION: VIRA
TITLE OF INVENTION: ASSC
TITLE OF INVENTION: ASSC
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                                                  TTACAGGAAAAGGCTTCTGAAATCAGACAATGCCTTTCAAACTCT-----TATACCAAC
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                                                                                  GGGGAAGAATGCTGTTAGTATGTTAATCTGGAATCATTACTGAGAAAGTTAAAGAA 121
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                                                                                                                     GGGGTAGAGTGTTTTTTTATACTAACCAGTCAGGATAATATGAGATACCACCCAGTGT
      CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA
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APPLICANT: Choo, Losinee
APPLICANT: Cancilla, Michael R.
TITLB OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT APPLICATION NUMBER: US/09/078,294
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 850 ID NOS: 29
LENGTH: 80595
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llarity 58.5%; Pred. No. 6.5e-40;
Conservative 0; Mismatches 214;
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Best Local Similarity
Matches 327; Conserv
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1431 TTACTCGCCTTTGGGCCCTGTATTTTTAACCTCCTTGTCAATTTGTTTCTTCTAGGATC 1490
                                                                                                                   CAAAACCGTCAAGGCCTAGACCTCCTCACTGCTGAAAGGAGGACTCTGCACCTTCTTA 1256
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                                                                                2 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA
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  Score 165; DB 4; Length 1859;
Pred. No. 1.4e-45;
0; Mismatches 247; Indels 17;
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APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Da Sart, Desiree
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6265211
GENERAL INFORMATION:
12.4%;
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ORGANISM: Nucleotide sequence
                      Best Local Similarity 58.3
Matches 369; Conservative
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Best Local Similarity 58.7
Matches 360; Conservative
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LENGTH: 80246
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US-09-078-294-4
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    Query Match
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APPLICANT: JOSN, HEE-SOOK
APPLICANT: PARK, HAE-JOON
APPLICANT: AHN, JONG-SEONG
APPLICANT: AHN, JONG-SEONG
APPLICANT: AHN, YOUNG-JU
APPLICANT: HA, YOUNG-JU
APPLICANT: CHUNG, SOO-IL
FILE PERRENCE: 98-338
CURRENT APPLICATION NUMBER: US/09/120, 653D
CURRENT FILING DATE: 1998-07-22
PRIOR PILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Kopatentin 1.71
SEQ ID NO 1
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50 GCTAAAGGCTTGCCATTGTTCCTGCACGGCTAAGTKWMKKGSYTKGKTYT
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8.1%; Score 107.8; DB 3;
Best Local Similarity 56.5%; Pred. No. 9.6e-26;
Matches 308; Conservative 0; Mismatches 217;
                                                                                                                                                                                                                   Sequence 1, Application US/09120653D Patent No. 6365727
                                                                                                                                                                                                                                                                                                                                 APPLICANT: YOON, JI-WON APPLICANT: JUN, HEE-SOOK
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           116 AAAGAAATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGG 175
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82.4%; Pred. No. 8.7e-32;
tive 10; Mismatches 19;
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Patent No. 6639063
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
ITLE OF INVENTION: ESTS and Encoded Human Profile REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
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ORGANISM: Homo sapiens
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SEQ ID NO 2599
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Best Local S
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Best Local Similarity 55.1
Matches 190; Conservative
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; LOCATION: (382)..(1995)
US-09-799-451-249
                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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     Sequence 24228, Application US/0951399C

Sequence 24228, Application US/0951399C

Sequence 24228, Application US/0951399C

SENERAL INFORMATION:
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REPERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT PILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 24228

LENGTH: 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Indels
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Pred. No. 3.7e-25;
2; Mismatches 15
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Patent No. 6783969
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Yamazaki, Victoria
Chen, Rui-hong
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US-09-513-999C-24228
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Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
Ren, Feiyan
Zhang, Jie
Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
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Best Local Similarity 87.1
Matches 122; Conservative
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LOCATION: 129
OTHER INFORMATION: n=a,
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                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 127
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-09-513-999C-24228
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APPLICANT: NAZERIAN, KEYVAN
APPLICANT: CALVERT, JAY G.
APPLICANT: CALVERT, JAY G.
APPLICANT: WITTER, RICHARD L.
APPLICANT: WITTER, NOBORD L.
TITLE OF INVENTION: VACCINE COMPRISING FOWLPOX VIRUS
TITLE OF INVENTION: RECOMBINANTS EXPRESSING THE ENVELOPE GLYCOPROTEIN OF AN
TITLE OF INVENTION: AVIAN RETICULOENDOTHELIOSIS RETROVIRUS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1683 AGATGAAAATGTTGCTTTTGGGTAAATCAATCAGAAAAGTACAAGACAACATCAGACA 1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  803 AGGAACTTGGAAATGGTTCTTTGGGTTCTTCCCCTTACAGGCCCACTTGTTAGTCTCCT 1862
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APPLICANT: Ghosh, Reena

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 678395921 Nucleic Acids and

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 803

CURRENT APPLICATION NUMBER: US/09/799,451

CURRENT PLILMS DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 948

SOFTWARE: DE_F_Genes Version 2.0

SEQ ID NO 249
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.7e-18;
0; Mismatches 152;
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Patent No. 5403582
GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: RD114
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US-09-555-352-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 ATTTGAGATCGAATATAATGTAGAGCAGGGACCTTCAAAACACTGCACCCTGGGGCCTC 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 80.6; DB 1; Length 1
Pred. No. 1.1e-16;
0; Mismatches 144; Indels
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APPLICANT: Collins, Mary KL
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
BARLIER APPLICATION NUMBER: PCT/GB96/02061
BARLIER PILING DATE: 1996-08-23
EARLIER PILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,282B
FILING DATE: 19930121
CLASSIFICATION: 424
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Sequence 1, Application US/09011745
Patent No. 6165715
GENERAL INFORMATION:
                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1644
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                         TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n 6.1%;
Similarity 53.7%;
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US-08-007-282B-1
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LENGTH: 2518
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Best Local
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                                                                                                                                                                                                            Query Match 6.1%; Score 80.6; DB 3; Length 2518; Best Local Similarity 53.7%; Pred. No. 1.5e-16; Matches 167; Conservative 0; Mismatches 144; Indels 0
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; Batent No. 654479;
; CENERAL INFORMATION;
; APPLICANT: Cichutek, Klaus
; APPLICANT: Cichutek, Klaus
; APPLICANT: Merget-Millitzer, Heike
; TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH
; TITLE OF INVENTION: MODIFIABLE SURFACE CAPSID PROTEINS
; FILE REFERENCE: 11692-005001
; CURRENT APPLICATION NUMBER: US/09/555,352
CURRENT FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: DE 197 52 855.4
; PRIOR PILING DATE: 1998-11-27
; PRIOR FILING DATE: 1998-11-27
; RIOR PILING DATE: 1998-11-27
; SRQ ID NOS: 34
; SGQ ID NOS: 34
; SGCTWARR: FaetSEQ for Windows Version 4.0
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53.7%; Pred. No. 2.4e-16;
live 0; Mismatches 144; Indels
FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)

OTHER INFORMATION: n is any nucleotide
US-09-011-745-1
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Best Local Similarity 53.74
Matches 167; Conservative
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2788 CAAAATTAGGAGGGACTGGACCTACTAACGGCAGAACAAGGAGGAATTTGTTTAGCCTTA 2847
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                                                                                    Length 5865;
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                                                                                  Score 80.6; DB 3; Length 5 Pred. No. 2.7e-16; 0; Mismatches 144; Indels
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Pred. No. 3.1e-16;
0; Mismatches 158;
; LOCATION: (3802)
; OTHER INFORMATION: n is any nucleotide US-09-011-745-8
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Best Local Similarity 55.9%;
Matches 213; Conservative
                                                                                    Query Match 6.1%;
Best Local Similarity 53.7%;
Matches 167; Conservative
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                                       .526 crccaadaggaccrrarcgagadaaakgrocrocreracadaaaccoccrorocoga 1585
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122 ATTIGAGAICGAATAIAATGIAGAGCAGAGGACCTICAAAACACIGCACCCIGGGGCCIC 181
                                                                                                                                                                  TTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAATT 301
                                                                                  182 CTCAGCCAATGGATGCCCTGGACTCTCCCCTTTAGGACCTCTAGCAGCTATAATTT
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Patent No. 6165715
GENERAL INFORMATION:
APPLICANT: COllins, Mary KL
APPLICANT: Collins, Mary KL
APPLICANT: Heiss, Robin A
APPLICANT: Casect, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1995-08-23
EARLIER FILING DATE: 1995-08-23
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LOCATION: (3612)
OTHER INFORMATION: n is
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LOCATION: (3613)
OTHER INFORMATION: n is
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LOCATION: (361<u>4)</u>
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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NAME/KEY: misc_feature
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LOCATION: (3800)
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LOCATION: (3801)
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SEQ ID NO 8
LENGTH: 5865
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US-09-011-745-8
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1230 AANGTGAGGCTTGCCACCATTTGGGAAGTGGCCCACTGCCATTTTGGTAGCGGCCCACCA 1289
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APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENEST. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 17982
LENGTH: 442
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
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Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunqing
Mang, Punging
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US-09-621-976-17982
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Matches 83; Conserv
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                                                                                                                                                        TIACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAATT 301
                                                                                                                                                                                                                                     Tracticgccirricgccccagcarritraacgircricrcaaarricr-rrercragarrc 380
                                                                                                                                                                                                                                                                                                                 GAAGCTGTAAAACCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAAA 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 -----ACTAGCCTAAAAGTTCCCCTCTGGAGGACACCACCAACTGCAGGGCCCCT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           520 ACTTGGGTTTTCCTGTTGAGAGGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGC 579
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                                                                            crerecrecesca a carecricio a contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra c
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        CTCAGCCAATGGATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATTT
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59.2%; Pred. No. 1.8e-15;
tive 0; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11057, Application US/09621976.

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Obsert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1057
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US-09-621-976-17982
US-09-621-976-17982
; Sequence 17982, Application US/09621976
; PATENT No. 6619063; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCTACCGTGGACCCCTGGAC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 Trcracegaegacaccregac 461
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Matches 190, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-11057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
ITILE OF INVENTION: POLYPEPLIGES
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312B
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL-Genes Version 1.0
LENGTH: 2809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.2%; Score 69.6; DB 4;
Best Local Similarity 55.8%; Pred. No. 9.6e-13;
Matches 154; Conservative 0; Mismatches 119;
Sequence 171, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
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Search completed: January 22, 2005, 19:37:03 Job time : 127.063 secs

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2005, 12:12:40 ; Search time 721.788 Seconds (without alignments) 10579.682 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                              January 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 108, App	Sequence 108, App	Sequence 81, Appl	Sequence 910, App	Sequence 17, Appl	Sequence 18, Appl	Sequence 9936, Ap	Sequence 4, Appli	Sequence 134, App	Sequence 3, Appli	Sequence 1, Appli	Sequence 30, Appl
	σı	US-08-979-847-108	US-10-114-104-108	US-09-873-367C-81	US-10-087-192-910	US-10-220-120-17	US-10-637-565-18	US-10-198-846-9936	US-10-416-642-4	US-10-114-893-134	US-10-016-249-3	US-09-902-535-1	US-10-632-793-30
	DB	80	15	10	13	16	16	14	16	13	15		16
	Query Match Length DB ID	1329	1329	56093	21646	1393	2030	7974	2074	2946	2946	2930	7582
dР	Query	99.8	99.8									55.0	
	Score	1326	1326	1035.2	798.2	778.8	775.4	774.2	766.8	731.8	731.8	730.8	722.6
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Sequence 25, Appl	Sequence 26, Appl	Sequence 1, Appli	4444,	730,	Sequence 385, App	34, 7	Sequence 6, Appli	Sequence 9, Appli	Seguence 1, Appli	Sequence 1102, Ap	~	102		679	Sequence 2833, Ap	Sequence 3, Appli	Sequence 3, Appli	7065,	Sequence 6815, Ap	67	Sequence 28, Appl	14	16	Seguence 98772, A	9	ñ	Sequence 14, Appl	ŭ	294 6	21,	20,	Seguence 1148, Ap
5 US-10-632-793-25			US-09-864-761-4444	3 US-10-087-192-730				3 US-10-003-806-9		5 US-10-240-425-1102	US-08-979-847-102	5 US-10-114-104-102	5 US-10-220-120-15	3 US-10-719-993-6792	5 US-10-264-237-2833	US-09-731-231A-3	7 US-10-751-985-3	₽				1 US-09-997-722-148	3 US-10-087-192-1666	3 US-10-027-632-98772	5 US-10-027-632-98772	5 US-10-637-565-1		US-09-864-761-7501			5 US-10-632-793-20	5 US-10-104-047-1148
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54.3	53.6	53.5	53.0	48.4	48.0	45.3	43.6	43.6	42.9	41.0	41.0	41.0	40.3	39.9							35.0				34.4	m	m	٦.	33.4	33.1	33.1	33.0
721.2	712.6	711	704.8	643.4	637.8	601.4	579.8	579.8	570.2	545.4	545	545	536.2	530.6	512	502	502	478.6	478.6	468.8	465	465	460	457.8	457.8	455.8	455.8	453.6	444	440.4	440.2	438
13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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US-08-979-847-108

i Sequence 108, Application US/08979847

publication No. US20030039664A1

GENERAL INFORMATION:

APPLICANT: BESEME, FREDERIC

APPLICANT: BESEME, FREDERIC

APPLICANT: BESEME, FREDERIC

APPLICANT: ROWURIAN-PRADEL, FLORENCE

APPLICANT: CANTON: COLETTE

APPLICANT: GARANGO-BACCALA, GLAUCIA

APPLICANT: GARANGO-BACCALA, GLAUCIA

APPLICANT: TUKE, PHILIP

APPLICANT: GARSON, JERRAY

APPLICANT: TUKE, PHILIP

TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS

TITLE OF INVENTION: THERAPEUTIC PURPOSES

NUMBER OF SEQUENCES: 210

CORRESPONDENCE ADDRESS: 210

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: ASTRET: VA

STREET: P.O. BOX 19928

CITY: ALEXANDRIA

STREET: VA

COUNTY: VALEXANDRIA

ZIP: 22220

COMPUTED PUTTER

COMPUTED PUTTER

ZIP: 22220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847 FILING DATE: 26-NOV-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
THERAPEUTIC PURPOSES
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/10/114,104
FILING DATE: 03-Apr-2002
CLASSIFICATION: <unimoderate the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the 
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US-10-114-104-108
; Sequence 108, Application US/10114104
; Publication No. US20030198647A1
; GENERAL INFORMATION:
; APPLICANT: PERROW, HERVE
; BESEME, FREDERIC
BEDIN, FREDERIC
; PARANHOS-BACCALA, GLI
KOMMINIAN-PRADEL, FLO
KOMMINIAN-PRADEL, FLO
KOMMINIAN-PRADEL, FLO
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ADDRESSEE: OLIFF & BERRI
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
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COMPUTER READABLE FORM:
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100.0%; Pred. No. 0;
iive 0; Mismatches
NAME: BERRIDGE, WILLIAM P.
REGISTRATION VIMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPRIONE: 703-836-6400
TELEPRIONE: 703-836-2787
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           LENGTH: 1329 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 1329; Conservative
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
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GENERAL INFORMATION:

APPLICANT: Young, Paul
APPLICANT: Soppet, Daniel
APPLICANT: Endress, Gregory
APPLICANT: Endress, Gregory
APPLICANT: Endress, Gregory
APPLICANT: Endress, Gregory
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REPRENCE: 689290-64
CURRENT FILING DATE: 2003-04-29
FRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/236,892
PRIOR FILING DATE: 2000-09-29
FRIOR FILING DATE: 2000-01-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
SEQ ID NOS: 1067
SOFTWARE: PatentIn version 3.0
SEQ ID NO 81
TYPE: DNA
                                                                                                                                                                                                                                                                                                                            961 GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGT 1020
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                  AATCATCTATTGCCTGAGAGCACAGGGGAAAGAACAAGGATTGGGATATAAACTCAGGCA 780
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            ATTORNEY ON NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
ATTORNEY/ANG DATE: 26-NOV-1997
NAME: BERRIDGE, WILLILAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-787
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                        99.8%; Score 1326; D
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: CDNA; SEQUENCE DESCRIPTION: SEQ ID NO: 108: US-10-114-104-108
                                                                                                                                                                                                                                       LENGTH: 1329 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 1329; Conservative
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37966 GCTGACTCCCATCCCTCTGGATCATGCAGGTGTCCGCTGTGCTCCTGATCCAGCGAGGC 38025
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                                                  AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGGGAAGGTGACC
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                                                                                                                                                                                                                                                                                                                                  Sequence 910, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Morris, David W.
TITLE OF INVENTION: GNACER
TITLE OF INVENTION: GNACER
TITLE OF INVENTION: GNACER
FILE REFERENCE: 52945200012
CURRENT FILING DATE: 2002-01
PRIOR APPLICATION NUMBER: US 99/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 910
LENGTH: 21646
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OTHER INFORMATION: n = A, T, C or G
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FEATURE:
NAME/KEY: misc_feature
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US-10-087-192-910
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                                                                                   Gaps
                                                    Length 56093;
                                                                                  13;
                                                  Score 1035.2; DB 10; Lengtl
Pred. No. 9.7e-311;
0; Mismatches 111; Indels
                                                  77.9%;
                                                    Query Match
Best Local Similarity 90.1
Matches 1133; Conservative
      ORGANISM: Homo sapiens
          ; OKGANISM: HOM
US-09-873-367C-81
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60/184,770; 60/184,774;
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APPLICANT: Will Jimmy Y.

APPLICANT: BRADLEX, Diana L.

APPLICANT: BRADLEX, Shawn R.

APPLICANT: BRADLEX, Shawn R.

APPLICANT: GRIEN, Wensheng

APPLICANT: GHEN, Wensheng

APPLICANT: COHEN, Howard J.

APPLICANT: CHEN, Wensheng

APPLICANT: LINCOLN, Stephen B.

APPLICANT: LINCOLN, Stephen B.

APPLICANT: JACKSON, Stuart

COURRENT APPLICATION NUMBER: US/10/220,120

COURRENT PILING DATE: 2002-06-27

COURRENT APPLICATION NUMBER: G0/184,777; G0/184,797; G0/184,776;

G0/184,709; G0/184,711; G0/184,813; G0/184,776;

G0/184,709; G0/184,711; G0/184,817; G0/184,776;

G0/184,709; G0/184,711; G0/184,817; G0/184,817; G0/184,911;

G0/204,815; G0/205,285; G0/205,232; G0/205,223; G0/205,221;

G0/204,815; G0/205,286; G0/205,282; G0/205,232; G0/205,287;

G0/204,815; G0/205,286; G0/205,282; G0/205,232; G0/205,241; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-16; 2000-02-16; 2000-05-16; 2000-05-17;

NUMBER OF SEQ ID NOS: 422

SEQ ID NO 17

LENGTH: 1393

LENGTH: 1393
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                                                                                        ROSEN, Bruce H.
RUSSO, Frank D.
STOCKDREHER, Theresa K.
DAFFO, Abel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: unsure
LOCATION: 120, 765
OTHER INFORMATION: a, t, c, g, usure.
                      JONES, Anissa L.
LIU, Tommy F.
ROSEBERRY, Ann M.
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OTHER INFORMATION: Incyte
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ORGANISM: Homo sapiens
  HILLMAN,
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APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: SPIRO, Peter A.; APPLICANT: BANVILLE, Steven C.
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CHALUP, Michael S.
CHALUP, Michael S.
CHEN, Alice
D'SA, Steven A.
AMSHEY, Stefan
DAHL, Christopher R.
DAN, Tam C.
DAN Tam C.
DUROUR, Gerard E.
FLORES, Vincent
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APPLICANT:
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; PRIOR FILING DATE: 1999-02-15 ; NUMBER OF SEQ ID NOS: 20 ; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 18 ; LENGTH: 2030 ; TYPE: DNA ; ORGANICM: MSRV-1 retrovirus ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)(1626) US-10-637-565-18 Guery Match Gest Local Similarity 92.8%; Score 775.4; DB 16; Length 2030; Best Local Similarity 92.8%; Pred. No. 1:9e-230; Matches 812; Conservative 0; Mismatches 63; Indels 0; Gaps 0;	1 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGGAACCTGTTAA	Oy 181 CCTCAGCCAATGGATGCCCTGGACTCTCCCTTTTAGGACCTCTAGCAGCTATAATATT 240 Db 1320 CCTCAGCCAATGGATGCCTTGGATTCTTTTTTTTTTTT 1379 Qy 241 TTTACTCCTTTTGGACCTTGTACTTCTTTTTTTTTTTTT		QY	
240 CGGGGACTGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTA 299 602 NCTGGGAAGGTGACCGCATCCATCTTAAACATGGGGCTTGCAACTTAGCTCACACCCGA 661	CCCAAGCAITCGAGCCAGCAACGGCTGCCCCTTTGTGTCCCCTCTTTGTATGGGAGC TCTGTTTTCACTCTATTTCACTCTATTAAATCATGCACTCTCCCTTTTGTATGGGAGC TCTGTTTTCACTCTATTTCACTCTATTAAATCATGCACTCTCTCT	650 GACCTGCCGCTGACTTCTTTTTTTTTTTTTTTTTTTTTT	1133 TCCATGACCACGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATT 1192	949 GGAAGTGGCCTGCCCCATTTTGGAAGTGGCCTGCCATCTTGGGAGCTCTGGGAGCA 1008 1313 AGGATCCCCCAGTAACA 1329 1009 AGGACCCCTGGTAACA 1025	SEULT 6 Sequence 18, Application US/10637565 Publication No. US20040043381A1 GENERAL INFORMATION GENERAL INFORMATION APPLICANT: PERRON, Herve APPLICANT: PERRON, Herve APPLICANT: KOMURIAN-PRADEL, Florence TITLE OF INVENTION: THE LTR REGION OF MSRV-1 RETROVIRUS FILE REFERENCE: 110257 CURRENT APPLICATION NUMBER: US/10/637,565 CURRENT FILING DATE: 2003-08-11 PRIOR APPLICATION NUMBER: US/19/9890,340 PRIOR APPLICATION NUMBER: PCT/1B00/00159 PRIOR APPLICATION NUMBER: PCT/1B00/00159 PRIOR FILING DATE: 2000-02-15 PRIOR APPLICATION NUMBER: EP 99420041.8

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     838 TITCACTCTAITTCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc feature
OTHER INFORMATĪON: Incyte ID No. US20040043452Al 7477736CBl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: RAWKUMAR, Jayalaxmi
APPLICANT: ARVIZU, Chandra
ITILE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
FILE REFERENCE: PF-0842 PCT
CURRENT APPLICATION NUMBER: US/10/416,642
CURRENT APPLICATION NUMBER: 05/249,407
PRIOR APPLICATION NUMBER: 60/249,407
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL PROGram
SEQ ID NO 4
LENGTH 2074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: a, t, c, g, or other US-10-416-642-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/10416642; Publication No. US20040043452A1; GENERAL INFORMATION:
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youchen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
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Pred. No. 9.2e-230;
0; Mismatches 126; Indels
1980 CACTCTATTTCACTCTATTAAATCTTGCAACTGAA 2014
                                                                                                                                                                                                                                                                                                        FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING BATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9936
                                                                                                                   ; Sequence 9936, Application US/10198846; Publication No. US20030099974A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.3%;
85.8%;
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Best Local Similarity 85.8
Matches 937; Conservative
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ORGANISM: Homo sapiens
US-10-198-846-9936
                                                                                 RESULT 7
US-10-198-846-9936
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APPLICANT: Kelleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM FILE REFERENCE: GI 6000-10A
CURRENT PILING DATE: 2002-04-02
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: PARENTING VET: 2.0
SEQ ID NO 134
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Pred. No. 9.1e-217;
0; Mismatches 69;
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Best Local Similarity 90.7%;
Matches 794; Conservative
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US-10-114-893-134
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                                                                                                                                                                                            CCTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTT
                                                                                                                                                                                                                                                                       1443 GTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAAT
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                                                                                                  AATTTGAGATCGAATATAATGTAGAGCAGACCTTCAAAACACTGCACCCTGGGGCCT
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Publication No. US20020193567A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Wears, Cheryl
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaniding, Vikki
APPLICANT: Spaniding, Vikki
APPLICANT: Carlin-Duckett, McKeough
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US-10-114-893-134
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RESULT 11
US-09-902-535-1; Sequence 1. Application US/09902535
; Patent No. US20020102530A1
; GENERAL INFORMATION:
; APPLICANT: Weith, Jr., James C.;
; APPLICANT: Mi, Sha
; TITLE OF INVENTION: Methods and compositions for diagnosing
; TITLE OF INVENTION: Methods and compositions for diagnosing
; TITLE OF INVENTION: Methods and compositions for diagnosing
; TITLE OF INVENTION: Methods and compositions for diagnosing
; TITLE OF INVENTION: Methods and compositions for diagnosing
; TITLE OF INVENTION: Moscres
; FILE REFERENCE: GIN-6006B4
; CURRENT FILING DATE: 2001-07-09
; PRIOR PILING DATE: 2001-07-09
; PRIOR PILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PastEEQ for Windows Version 4.0
; SEQ ID NO
                                                                                             2654
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                                                                                                                                                                     2655 Agcrigadadagardaccacarccacrirraaacacagagcrirgcaacriaacrcaacarg
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                                                                                                                                      601 ANCTGGGAAGGTGACCGCATCCATCTTAAACATGGGGCTTGCAACTTAGCTCACACCCG
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                                                            541 GGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
                                                                                                                                                                                                            661 ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC
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Pred. No. 1.9e-216;
0; Mismatches 69;
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Best Local Similarity 90.7%;
Matches 793; Conservative
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; LOCATION: (930)...(2546)
US-09-902-535-1
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).le-217;
                                                                          2895 CATGCTATTTCACTCTATTAAATCTTGCAACTGCA 2929
                                                        841 CACTCTATTCACTCTATTAAATCATGCAACTGCA 875
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; Pred. No. 9.1e-
0; Mismatches
                                                                                                                                                                                     Sequence 3, Application US/10016249
Publication No. US20030100053A1
GENERAL INFORMATION:
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Best Local Similarity 90.7%;
Matches 794; Conservative
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ORGANISM: Homo sapiens
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US-10-016-249-3
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Best Local Similarity 88.5%; Pred. No. 1.1e-213;
Matches 774; Conservative 19; Mismatches 70
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LOCATION: (2398)..(2398)
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NAME/KEY: misc feature
LOCATION: (307)..(307)
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LOCATION: (3787)..(378'
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ORGANISM: Homo sapiens
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PUblication No. US20040048298A1

GENERAL INFORMATION

APPLICANT: PARANHOS-BACCALA, Glaucia

APPLICANT: MALLET, Francois

APPLICANT: WOISSET, Cecile

TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT

TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT

TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT

TITLE OF INVENTION: AUTOIMMUNE US/10/632,793

CURRENT FILING DATE: 2003-08-04

PRIOR FILING DATE: 2001-10-22

PRIOR PRIOR PLILING DATE: 2001-10-22

PRIOR PELICATION NUMBER: PT/FR00/00144

PRIOR PELICATION NUMBER: FR 99/00888

PRIOR FILING DATE: 1999-01-21
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APPLICANT: PARANNOS-BACCALA, Glaucia

APPLICANT: PARANNOS-BACCALA, Glaucia

APPLICANT: MALLET, Francois

TITLE OF INVENTION: AUTOINMUNE DISEASE, LABELING METHOD AND REAGENT

TITLE OF INVENTION: AUTOINMUNE DISEASE, LABELING METHOD AND REAGENT

TITLE OF INVENTION: AUTOINMUNE DISEASE, LABELING METHOD AND REAGENT

TITLE OF INVENTION: AUTOINMUNE DISEASE, LABELING METHOD AND REAGENT

CURRENT APPLICATION NUMBER: US/10/632,793

CURRENT FILING DATE: 2001-0-22

PRIOR FILING DATE: 2000-01-22

PRIOR PILING DATE: 2000-01-22

PRIOR PILING DATE: 2000-01-21

PRIOR FILING DATE: 1999-01-21

PRIOR FILING DATE: 1999-01-21

WUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN VETSION 3.1

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Matches 787; Conservative
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ORGANISM: Homo sapiens
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US-10-632-793-25
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                                                                                     Length 2782;
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                                                                                   53.6%; Score 712.6; DB 16;
89.4%; Pred. No. 8.7e-211;
ive 0; Mismatches 81; 1
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                                                                                                  Best Local Similarity 89.4
Matches 782; Conservative
                            TYPE: DNA
CORGANISM: Homo sapiens
US-10-632-793-26
Q ID NO 26
LENGTH: 2782
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RESULT 15 US-10-133-036-1

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Sequence 1, Application US/10133036
) Publication No. US20040054133A1
) GENERAL INFORMATION:
) APPLICANT: Conrad, Bernard
) APPLICANT: Mach, Bernard
) TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen
) FILE REFERENCE: 23138-507
) CURRENT APPLICATION NUMBER: US/10/133,036
) CURRENT FILING DATE: 2002-04-26
) PRIOR APPLICATION NUMBER: PCT/EPO0/10659
) PRIOR FILING DATE: 2000-10-30
) NUMBER OF SEQ ID NOS: 21
) SEQ ID NOS: 21
) SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2782;
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Pred. No. 2.7e-210;
0; Mismatches 82;
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Best Local Similarity 89.3%;
Matches 781; Conservative
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                                                                                                                                                                                                       9.
                                                                                                                                                               Length 1894;
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FETAL LIVER, SIGNAL = 6
1 ADULT LIVER, SIGNAL = 6
1 BRAIN, SIGNAL = 6.2
1 BONE MARROW, SIGNAL = 6
1 LUNG, SIGNAL = 3.9
1 HELA, SIGNAL = 7.2
                                                                                                                                                             Score 704.8; DB 9;
Pred. No. 1.9e-208;
0; Mismatches 79;
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                                                                                                                                                               Query Match
Best Local Similarity 89.7%;
Matches 770; Conservative
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US-09-864-761-4444
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Sequence 4444, Application US/09864761

FREENEN US US2002004733A1

GENERAL INFORMATION:
FREENEN US US2002004473A1

SPECIAL NO. US200200473A1

SPECIAL NO. US200200473A1

SPECIAL NO. US200200473A1

FREENEN SERVER SEGUENCE OF THE SERVER SINCLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXERESION ANALYSIS BY MICROARRAY TITLE OF INVENTION: GENE EXERESION ANALYSIS BY MICROARRAY THE REFERENCE: Aconica X-1

CURRENT PELICATION NUMBER: US/09/864,761

SPECIAL SEGUENCE ACONICA X-1

CURRENT APPLICATION NUMBER: US/09/864,761

PRIOR PLING DATE: 2001-05-204

FRIOR PLING DATE: 2000-05-204

FRIOR PLING DATE: 2000-05-204

FRIOR PLING DATE: 2000-05-204

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                                        2610 AATCATTTATTGCCTGAGAGCACAGGAGGACAATGATCGGGGATATAAACCCAAGTT
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OTHER INFORMATION: MAP TO AC002346.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = OTHER INFORMATION: EXPRESSED IN HELIO, SIGNAL = 6 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.4 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.9
                                                                                                                    Engine vers. 1.1
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SOFTWARE: Annomax Sequence Listing
SEQ ID NO 4444
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US-09-864-761-4444
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100298 TITCTAGGCCGACTAAGAATCCCAAAGCTAGCTAGGCAAGGTGACCACATCCACCTTA 100239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 48.0%; Score 637.8; DB 10; Length 780; Best Local Similarity 90.0%; Pred. No. 9.5e-188; Matches 711; Conservative 0; Mismatches 60; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100004 AATATTGCAACTGCA 99990
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NAME/KEY: rerpeat_region
LOCATION: (1)..(780)
OTHER INFORMATION: 1trl7
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Best Local Similarity 85.4%; Pred. No. 3e-188;
Matches 781; Conservative 0; Mismatches 88; Indels 46; G
                           WS-10-087-192-730/c

Sequence 730, Application US/10087192

Publication No. US2002182586A1

GENERAL INFORMATION:
APPLICANT: Morris, David W.
TITLE OF INVENTION: OVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: ONCE. COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
CURRENT APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 2059

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 730

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LOCATION: (1).T.(161334)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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US-10-087-192-730
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MS-09-864-867-385

Sequence 385, Application US/09854867

Sequence 385, Application Wo. US2003022435641

PUBLICATION No. US20030224356A1

GENERAL INFORMATION:

APPLICANT: ROGAN, PETER K

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING

TITLE APPLICATION UNMBER: US/09/854,867

CURRENT PELING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 613

SEQ ID NO 385

SEQ ID NO 385

LENGTH: 780 100058 crrcririassricccriccrrratarassssasscricrcr-----Grcrrcratra 100005 100178 AAATGCTAATTAGACAAAAAAGGGTAAAAAAATAGCCAATCATCTATCGCCTGAGAG 100119 100118 CACAGCGGGAAGGACAATGATCGGGATATAAACCCAGGCATTCAAGCCGGCAACGGCTAC 100059 2 667 180 899 608 61 AGGTGACCGCTTCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCCGACCAATCA 120 719 779 839 181 CAATCATCTATCGCCTGAGAGCACAGGGGGGGGACAATGATCGGGATATAAACCCAGGC 240 241 Arrica Accesca Accestración reservidades controlas de contra d 9 681 AAATGCTAATCAGCAAAAACAGGAGGTAAAGCAATAGCCAATCATCTATTGCCTGAGAG CACAGCGGGAAGGACAAGGATTTGGGATATAAACTCAGGCATTCAAGCCAGCAACAGCAAC 549 IGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGGGA 1 TGAGAGACAGGACTAGCTGGATTTCCTAGGCCGACTAAGAATCCCTAAGCTAGGTGGGA 609 AGGIGACCGCAICCAICTITAAACAIGGGGCTIGCAACTIAGCICACACCCGACCAAIC-668 -----AGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGC 720 CAATCATCTATTGCCTGAGAGCACAGCGGGAAGGACAAGGATTGGGATATAAACTCAGGC 780 ATTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTT 630 AACAIGGGGCTIGCAACTIAGCICACACCCGACCAAIC-----AGAGAGCICACIA CCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTCACTCTATTTCACTCTATTA 19;

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778 GCATTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGT
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Publication No. US20020119929A1

GENERAL INFORMATION:

APPLICANT: Blehop, Colin E.

APPLICANT: Agoulnik, Alexander I.

APPLICANT: Zhu, Qichao

TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY

TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY

FILE REFERENCE: PO2066U3/1/10024824

CURRENT FILING DATE: 2001-11-02

PRIOR APPLICATION NUMBER: 60/245,872

PRIOR FILING DATE: 2000-11-03

NUMBER: OF SEQ ID NOS: 14
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Matches 683; Conservative
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LENGTH: 180557
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US-10-003-806-6/c
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US-10-672-764A-34/C
; Sequence 34, Application US/10672764A
; Publication No. US20040156832A1
; GENERAL INFORMATION:
; AFPLICANT: JOILY, Chris
; TITLE OF INVENTION: Immunoglobulin Compositions and Methods
; FILE REFERENCE: 13311.1001U
; CURRENT APPLICATION NUMBER: US/10/672,764A
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84; Indels
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Pred. No. 3.8e-175;
0; Mismatches 84;
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al Similarity 87.0%;
689; Conservative (
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Best Local Similarity
Matches 689; Conserv
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TYPE: DNA
ORGANISM: Human
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Length 180557;
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Publication No. US20030124535A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Jeanette
TITLE OF INVEXTION: DIAGNOSIS AND TREATMENT OF VASCULAR DIS
FILE REFERENCE: MMI-008
CURRENT APPLICATION NUMBER: US/10/017,117
CURRENT APPLICATION NUMBER: No. US20030124535A1 yet assigned
PRIOR FILING DATE: 2001-12-05
                                 Indels
   DB 13;
Score 579.8; DB 13;
Pred. No. 2.2e-168;
0; Mismatches 90;
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86.0%;
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   Query Match
Best Local S:
Matches 683
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bishop, Colin E.

APPLICANT: Bishop, Colin E.

APPLICANT: Agoulnik, Alexander I.

APPLICANT: Adoulnik, Alexander I.

APPLICANT: Adoulnik, Alexander I.

TITLE OF INVENTION: CAN I AND ITS ROLE IN MAW

FILE REPERENCE: PO2066US1/10024824

CURRENT FILIAG DATE: 2001-11-02

PRIOR PILING DATE: 2000-11-03

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 9

LENGTH: 180557
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; ORGANISM: Human
US-10-003-806-9
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US-10-003-806-9/c
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                                                                                                                                              42.9%; Score 570.2; DB 15; Length 161671; 88.5%; Pred. No. 2.1e-165; ive 0; Mismatches 71; Indels 14; G
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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                                                                    FEATURE:
NAME/KEY: misc feature
LOCATION: (1). [(161671)
OTHER INFORMATION: n = a,t,c or
                                                                                                                                                                      Matches 655; Conservative
                                 LENGTH: 161671
TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 1102, Application US/10240425 Publication No. US20040033502A1

RESULT 23 US-10-240-425-1102

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54610 AATGAGAGACAGGACTAGCTGGATTTCCTAGGCCGACTAAGAATCCCTAAGCCTAGGCTGG 54669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
41.0%; Score 545.4; DB 16; Length 134292;
Best Local Similarity 85.9%; Pred. No. 1e-157;
Matches 680; Conservative 0; Mismatches 89; Indels 23; G
                                                      APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue FILE REFERENCE: 44921-5026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Genbank Accession No. US20040033502A1 AL031983
                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PATCHIN VET: 2.1
SEQ ID NO 1102
LENGTH: 134292
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
THERAPEUTIC PURPOSES
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61 CARATTGTTCTTCARATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC 120
                                                                                                                                                                                                 181 GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT 240
                                                                                                                                                                                                                                                                                       241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAAC 300
                                                                                                                                                                                                                                                                                                                                                                          301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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                                                                                                                                                                                                                                                 497 TGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTTCCTGTTGAGAGGGTGGACTGAGAGAC
                                                                                                                                                                                                                                                                                                                                  AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGGGAAGGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                       617 GCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGGCTC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATE: US-DOS/MS-DOS
FILING DATE: 03-Apr-2002
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BESBRA, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOWIRIAN-PRADEL, FLORENCE
JOLIVET-REYNAND, COLETTE
MANDRAND, BERNARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 102, Application US/10114104 Publication No. US20030198647A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESSS:
ADDRESSEE: OLIFF & BERRI
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         857 ATTAAATCATGCAACTGCA 875
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TUKE, PHILIP
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US-10-114-104-102
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TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: THERAPEUTIC PURPOSES
CORRESPONDENCES: 210
CORRESPONDENCE ADDRESS:
                                                                                                                                                             55316 CGGCCTGCGGCCATTTTGGAAGCAGCCCACCATCTTGAGAGCTCTGGGAGCAAAAGAC 55375
                                                                        55256 GAATCCATGAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTTGCCACCATCTTGGAAG 55315
                                                                                                                     TGGCCCACTGCCATTTTGGTAGCGGCCCACCACCATCTTGGGAGCTGTGGGAGCAAGGAT 1317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 CCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAATTGAAGCTGTAAAGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847
FILING DATE: 26-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Sequence 102, Application US/08979847
Publication No. US20030039664A1
GENERAL INFORMATION:
APPLICANT: BESEME, FREDERIC
APPLICANT: BESIN, FREDERIC
APPLICANT: BESIN, FREDERIC
APPLICANT: BARANHOS-BACCALA, GLAUCIA
APPLICANT: JOLIVET-REYNAUD, COLETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFRENCE/DOCKET NUMBER: WPB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 92.4
Matches 572; Conservative
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MEDIUM TYPE: Floppy
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CLASSIFICATION:
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US-08-979-847-102
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APPLICANT:
APPLICANT:
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APPLICANT:
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GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: PANZER, SCOLT R.
APPLICANT: BANVILLE, SCOCT R.
APPLICANT: SHAM, Purvi
APPLICANT: GHALUP, Michael S.
APPLICANT: CHALUP, Michael S.
APPLICANT: CHALUP, Alice
APPLICANT: CHANG, Simon C.
APPLICANT: CHANG, Simon C.
APPLICANT: DAML, Christopher R.
APPLICANT: DAML, Christopher R.
APPLICANT: DAM, Tam C.
APPLICANT: DAM, Tam C.
APPLICANT: DAMIELS, Susan E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGGACCAATCAGAGGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATTGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 635;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 545; DB 15;
Pred. No. 7.6e-159;
0; Mismatches 47;
        PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/979,847

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WEB 39046A

TELECOMMUNICATION INFORMATION:
TELEPAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
CLASSIFICATION: <Unknown>
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Best Local Similarity 92.4%;
Matches 572; Conservative
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                US-10-114-104-102
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; Sequence 15, Application US/10220120

RESULT 26 US-10-220-120-15

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60/184,698; 60/184,770; 60/184,774;
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; OTHER INFORMATION: Incyte ID No. US20040048253A1 LG:429446.1:2000FEB18
US-10-220-120-15
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APPLICANT: HICCLM, Stephen B.
APPLICANT: JACKSON, Stuart
ITILE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBENCE: PT-1113 PCT
CURRENT APPLICATION NUMBER: US/10/220,120
CURRENT FILING DATE: 2002-08-26
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Pred. No. 5e-156;
0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                    LIU, Tommy F.
ROSEBERRY, Ann M.
ROSEN, Bruce H.
RUSSO, Frank D.
STOCKOREHER, Theresa K.
DAFFO, Abel
                                                                                                                                                                               FONG, Willy T.
GREENAWALT, Lila B.
HILLMAN, Jennifer L.
JONES, Anissa L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRACHER, Shawn R.
CHEN, Wensheng
COHEN, Howard J.
DUFOUR, Gerard E. FLORES, Vince
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 81.4%;
Matches 650; Conservative
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or insertion/deletion polymorphism (see Tables 1-2
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                                                                                                                                                  257 CCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAATTGAAGCTGTAAAGCTA
                                                                      Length 366710;
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                                                                                                             Indels
                                                                          DB 18;
                                                                    Score 530.6; DB 18;
Pred. No. 7.3e-153;
0; Mismatches 56;
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; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT PILING DATE: 2002-10-04
; PRIOR PILING DATE: 2002-10-04
; PRIOR PILING DATE: 2000-05-18
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIN Ver. 3.1
; SEQ ID NO 2833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i LOCATION: (1)...(366710)
i OTHER INFORMATION: n = A,T,C or.G,
US-10-719-993-6792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTAAATCATGCAACTGCA 875
                                                                        Query Match
Best Local Similarity 91.0%;
Matches 563; Conservative
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US-10-719-993-6792/c

US-10-719-993-6792/c

Sequence 6792, Application US/10719993

Sequence 6792, Application US/10719993

Sequence 6792, Application No. US20040268849A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SOFTWARRE: FRANCES OF WINDOWS Version 4.0

SEQUID NOS: 57342
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                                                    GGGATTCTCCAAAGTGTTTTGTCTTTCCAGAATCAAAACTGTAAAACTACAAATTGTTCT 165
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                                                                                                                                                                       TGCTAGACTATGCTCTGATGTTAATGACATTGAAGTCACCCCTCCCGAGGAAATCTCAAC 447
                                                                                                                                                                                                          TGCTAGCCCATGCTCCGATGTTGATGACATCGAAGGCGCCCCTCCCAAGGAAATCTCAAC
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                                                                                                                              166 TCAAATGGAGCCCCAGATGCAGTCTATGACTAAGATCTACCACAGACCCTTGGACCGGCC
                                                                                                                                                                                                                                                                                                                       CTCCCCAACAGTACTTGGGTTTTCCTGTTGAGAGGGTGGACTGAGAGACAGGACTAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         761 TCACCATCCAGCAATGCTCTTTGCCACCATCACAGACCCGCCACTGACTTCCATCCCTCT
                     CAACTTCCTTGTTAAGTTTGTCTCCTTCCAGAATTGAAGCTGTAAAGCTACAAATAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTATGGCTCAAGCTGAGCTTTTTGT
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: NAME/KEY: misc_feature
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Sequence 3, Application US/10751985
Publication No. US20040126861A1
Publication No. US20040126861A1
APPLICANT: GUBGLER, Karl et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND UTILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND UTILE REPERENCE: CL001007CON
CURRENT APPLICATION NUMBER: US/10/751,985
CURRENT APPLICATION NUMBER: 2004-01-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 5.7e-144;
0; Mismatches 62;
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; SEQ ID NO 3
LENGTH: 326014
; TYPE: DNA
ROGANISM: Human
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(326014)
; OTHER INFORMATION: n = A,T,C or
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Best Local Similarity 88.7%;
Matches 557; Conservative
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US-10-751-985-3/c
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Sequence 3. Application US/09731231A
Patent No. US20020082189A1
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, ITILE OF INVENTION: THEREOF
FILE REPERENCE: CLOO1007
CURRENT APPLICATION NUMBER: US/09/731,231A
CURRENT PILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                               93; Indels 18;
                                            Length 17758;
                                        Score 512; DB 16;
Pred. No. 9.1e-148;
0; Mismatches 93;
                                        Query Match 38.5%;
Best Local Similarity 84.7%;
Matches 614; Conservative
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TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(326014)

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: January 22, 2005, 12:01:19; Search time 3958.84 Seconds (without alignments) 12232.983 Million cell updates/sec Title: US-09-319-1568-12 Perfect score: 1329 Sequence: 1 tcaaaatcgaagagctttaggcaaggatcccccagtaaca 1329 Scoring table: IDENTITY NUC Gapop 10-0, Gapext 1.0 Searched: 32822875.seqs, 18219865908 residues Total number of hits satisfying chosen parameters: 65645750	00000000 Match 0%	Processing: Minnum March 0% Listing first 45 summaries Listing first 45 summaries Listing first 45 summaries Listing first 45 summaries Listing first 45 summaries EST:* 1: 9b_est1:* 3: 9b_est2:* 3: 9b_est3:* 5: 9b_est3:* 6: 9b_est5:* 7: 9b_est6:* 8: 9b_est6:* 8: 9b_est6:* 7: 9b_est6:* 8: 9b_est6:* 9: 9b_gs2:* 9: 9b_gs2:* 9: 9b_gs2:* 9: 9b_gs2:* 9: 9b_gs2:* and is the number of results preserve greater than or equal to the sconand is derived by analysis of the tota	% Que: re Mate	!	500.6 37.7 1002 5 BX953822 BX52822 480.8 36.2 999 4 BM918330 AG113694 475.2 35.8 683 9 AG134524 AG134524 474 35.7 669 9 AGG49953 AGG49953 473 35.6 681 9 AGG49953 AGG49953 469.6 35.3 710 9 AGG96341 AGG96341 468.2 35.2 1160 3 BCG30968 BCG30968 465.2 35.0 893 5 BQ437925 BQ437925

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1916 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1976 AGGGAAGAATGCTGTTATTATGTTAATCAATCCGGAATGGTCACCTGAGAAAGTTAAAGA
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                 Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                     Cot 25-normalized"
                                                                                                                                                                                                                                                                                                                                                                                                                    52.9%; Score 702.8; DB 3; 90.4%; Pred. No. 1.8e-201; ive 0; Mismatches 69;
                                                                                                                                                                                                                                                                 1. 2749
/ Organism="Homo sapiens"
/ AD_xref="naxon:9606"
/ Cloine="CSODIO22Y13"
/ Lissue type="Plazerta Cot
/ plasnid="pocwysporr_6"
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les 765; Conservative
 Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, Wases I to 2749)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                        CCTCAGCCAATGGATGCCCTGGACTCTCTTAGGACCTCTAGCACCTATAATATT
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                                                                                AATITGAGATCGAATATAATGTAGAGCAGGACCTTCAAAACACTGCACCCTGGGGCCT
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DEFINITION
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Gaps

12; 2749;

Length Indels 2035

120

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2504 AGCTGGGAAGGTGACCACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTG

ANCTGGGAAGGTGACCGCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCG

601

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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE

CR617248

RESULT

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REFERENCE AUTHORS TITLE

Oy 181 CCTCAGCCAATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATAT 240	Qy 241 TTTACTCCTCTTTGGACCTGTATCTTCAACTTCCTTGTTTAGTTTGTCTCTTCCGAAT 300	Qy 301 TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 360	Oy 361 AATCTACCGTGGACCCCTGGACCGGCTGCTAGACTATGCTCTGATGTTAATGACATTGA 420	Qy 421 AGTCACCCCCCCGAGGAAATCTCAACTGCACACCCCTACTACACTCCCAATTCAGTAGG 480 L	Qy 481 AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA 540 Db 2137 AAGCAGTTAGAGCGGTCGTCGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA 2196	Qy 541 GGGTGGACTGAGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT 600 Db 2197 TGGGGGACTGAGAGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCT 2256	Qy 601 ANCTGGGAAGGTGACCGCATCCATCTAAAACATGGGGCTTGCAACTTAGCTCACCCG 660 2257 AGCTGGGAAGGTGACCACACTCACACTTAAAACACGGGGCTTGCAACTTAGCTCACACGTG 2316	Qy 661 ACCAATCAGAGACTCACTAAAATGCTAATCAGGCAAAAACAGGGGTAAAGCAATAGCC 720	Qy 721 AATCATCTATTGCCTGAGGGAGGGGAAGGGAGGGATTGGGATTGGGATTAGACTCAGGCA 780	781 TTCAAGCCAGCAACACCCCTTTGGGTCCCCTCCCATTGTATGGGGAGCTCTGTTTTTTTT	Db 2437 TTCGAGCGGCAACGGCAACCCCTTTGGGTCCCCTCTTGTATGGGAGCTCTGTTT 2496 Qy 841 CA 842	Db 2497 CA 2498	Z Z	KEYWORDS HTC; CNBLT CDNA. SOURCE SOURCE ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,	REFERENCE 1 (bases 1 to 2748) AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D. TITLE Full-length CDNA libraries and normalization		TITLE Direct Submission JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
Qy 661 ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGGGTAAAGCAATAGCC 720 	OY 721 AATCATCTATTGCCTGAGAGCACAGCGGGAAGGACTAGGGATATAAACTCAGGCA 780	QY 781 TTCAAGCCAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT 840 Db 2684 TTCGAGCCGCAACGGCAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGAGCTCTGTTTT 2743	Oy 841 CACTCT 846 Db 2744 CATGCT 2749	Т 3 175	LOCUS CR622175 2500 bp mkNA linear HTC 21-JUL-2004 DEFINITION full-length cDNA clone CS0DI051YM13 of Placenta Cot 25-normalized of Homo sapiens (human) ACCESSION CR622175	Σ	SS	TITLE FULL-LENGUN CUNA LIDIZILES AND NOTMALIZATION JOURNAL Unpublished REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600	REFERENCE 2 (bases 1 to 2500) AUTHORS Genoscope.		ို ဝင္ပ	was normalized. Library was constructed by Lile Technologies, a division of Invitrogen. FEATURES Location/Qualifiers	(C) / (C) /	Query Match Best Local Similarity 90.6%; Pred. No. 3.18-201; Matches 763; Conservative 0; Mismatches 67; Indels 12; Gaps 1;	OY 1 TCAAAATCGAAGAGTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTT 60	Qy 61 AGGGBABGATGCTGTTAGTATGTTAATCAATCTGGBATCATTACTGAGBAAGTTAAAGA 120 	Qy 121 AATTTGAGATGGAATATAATGTAGGGAGGCTCTTCAAAACACTGCACCCTGGGGGCCT 180

08-APR-2004

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Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1071)

2 Li, W.B., Gruber.C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

L Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30374869.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EWRY cedex - France

BR 191 91006 EWRY cedex - France

BR 191 91006 EWRY cedex - France

BR 191 Sequenceope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                     BX365066
BX365066 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI046YA18 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mrna" reference //mol_type="mrna" reference //mol_type="mrna" reference //mole="CSODIO46VA18" //clone="CSODIO46VA18" //clone itype="PLACENTA COT 25-NORMALIZED" //clone itype="PLACENTA COT 25-NORMALIZED" //note="lst strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              767 AGGGGAAGAATGCTGTTATTATGTTAATCAATCCGGAATCGTCACTGAGAAAGTTAAAGA
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      2690 TICGAGCCGGCAACGCCCTTTGGGTCCCCTCTTGTATGGGGAGCTCTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS1AI012ZC10NP1&c=4215.r. Location/Qualifiers
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Pred. No. 6.1e-196;
3; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                            BX365066.2 GI:46304105
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89.9%;
                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
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Best Local Similarity 89.9
Matches 755; Conservative
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                                                                                               RESULT 5
BX365066/c
                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                        ORGANISM
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- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATCATCTATTGCCTGAGAGCACAGGGGAAGGACAAGGATTGGGATATAAACTCAGGCA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781 TICAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTCAGCCAATGGATGCCCTGGATTCTCCCCCTTCTTAGGACCTCTAGCCAGCTATAATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGCACCCCTCCTGAGGAAATCTCAGCTGCACAACCTCTACTACGCCCCAATTCAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2510 AGCTGGGAAGGTGACCACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAGACAGGAGGTAAAGAATAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2222 CGAAGCTGTAAAACTA------CAAATGGAGCCCAAGATGCAGTCCAAGACTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGCAGTTAGAGCGGTCGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                       Score 699; DB 3; I
Pred. No. 2.6e-200;
                                                                                                                                                         1. .2748
/organism="Homo sapiens"
/mol_type="mknAn"
/db_xref="taxon:9606"
/clone="CS0D1044YK06"
/tissue_type="Placenta Cot 2?
/plasmid="pcMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Gaps

13;

120

708 180 648

768

9

240

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BX337769 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI051YM13 3-PRIME, mRNA sequence.
BX337769 GI:46272079
EST.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2152 GCTACTCCTCTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCTTCCAGAAT 2211
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                                                                                                                                                                                       1972 AGGGGAAGATGCTGTTATTATCTTAATCAATCCGGAATCGTCACTGAGAAGTTAAAGA
                                                                                                                                                                                                                                                      2032 AATTCGAGATCGAATACAACGTAGAGCAGAGGAGCTTCGAAACACTGGAACCTGGGGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  421 AGTCACCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACTACACTCCAATTCAGTAGG
1320 AGGCACCCTCCTGAGGAAATCTCAGCTGCACACTCTACTACTACGCCCCAATTCAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2380 AAGCAGTTAGAGCGGTCGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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                                                                                                                                                           AGGGGAAGAATGCTGTTAGTATGTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA
                                                                                                                                                                                                                        AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAAACACTGCACCTGGGGCCTT
                                                                                                                                                                                                                                                                                     181 CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT
                                                                                                                                                                                                                                                                                                                                                  241 TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT
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                                                                                            1 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTT
                                                              Gaps
                                                              12;
                                 Length 2716
                                                             Indels
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                             DB 3;
                               Score 678.6; DB 3;
Pred. No. 4.1e-194;
0; Mismatches 66;
                                 51.1%;
90.5%;
                               Query Match 51.1
Best Local Similarity 90.5
Matches 739; Conservative
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full-length cDNA clone CS0DE013Y120 of Placenta of Homo sapiens
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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                                                 GATCTACCGCAGACCCCTGGACCGCTGCTAGCCCACGATCTGATGTTAATGACATCAA
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                                                                                                                                                                                                                                                      <u>ANCTGGGAAGGTGACCGCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCG</u>
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                               AATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGATGACATTGA
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HOmo sapiens (human)
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Contaction, Buttheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1058)

11, W.B., Gruber, C., Jessee, J. and Polayes, D.

1 Full-length cDNA libraries and normalization

1 Unpublished (2001)

1 On May 8, 2003 this sequence version replaced gi:30439129.

1 Contact: Genoscope - Centre National de Sequencage

1 BP 191 91006 ENRY cedex - France

1 Email: seqrefegenoscope.cns.fr, Web: www.genoscope.cns.fr

1 Strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

1 end enriched, double-strand cDNA was digested with Not I and cloned

1 into the Not I and EcoR.V sites of the pCMVSPORT & vector. Library

1 was normalized. Library was constructed by Life Technologies, a

1 division of Invitrogen. This sequence belongs to sequence cluster
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COT 25-NORMALIZED Homo sapiens cDNA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/clone="Ist strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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           540 AGGGTGGACTGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCC
                                                         600 TANCTGGGAAGGTGACCGCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACCCC
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Pred. No. 6e-189;
); Mismatches 92;
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Matches 727; Conservative
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                                                                                                                                                                                                                                                                                             Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Li, Chases 1 to 998)
Li, W.B.; Gruber, C.; Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For more information about this cluster, see http://www.genoscope.cns.fr/cdna7s=CSODI051AG07NP1&c=4215.r.
                                                                                                                                                                                                                                   gi:30337641.
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                                                                                                                                                                                                                       On May 2, 2003 this sequence version replaced Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 669.4; DB 5;
Pred. No. 1.9e-191;
2; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI051XM13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Best Local Similarity 89.2%;
Matches 754; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           487
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                                                                                                                                                  TITLE
JOURNAL
                                                                             REFERENCE
                                                                                                                   AUTHORS
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cne.fr, Web : www.genoscope.cne.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-efrand cDNA was digested with Not I and Cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

This sequence belongs to sequence cluster 4215.r

For more information about this cluster, see
http://www.genoscope.cne.fr/cdna?s=CSODE012DE12NP1&c=4215.r.
                                                                                                                                                                                                                                                                      // Organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/dolone="CSODE012V124"
/tissue_type="PLACENTA"
/clone="Lebendo sapiens PLACENTA"
/note="Vector: pCWVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AGGGGAAGAAGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAAAAGTTAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGGGAAGAATGCTGTTACTAATCAATCCGGAATCGTCACTGAGAAAGTTAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          655 CCTCAGCCAATGGATGCCCTGGATTCTCCCCCTTCTTAGGACCTCTAGCAGCTATAATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  595 GCTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTTTCCAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAAGCTGTAAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 AATCTACCGTGGACCCCTGGACCGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           487 GATCTACCGCAGACCCCTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 TGGGGGACTGAGAGACAGGACTAGCTGGATYCCCYAGGCTGACTAAGAATCCCTAAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.1%; Score 652.2; DB 5;
llarity 85.5%; Pred. No. 3.2e-186;
Conservative 19; Mismatches 91;
                                                                                                                                                                                                                                                              1. .1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 725; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                    532 CGAAGCTGTAAAACTA-----CAAATGGAGCCCAAGATGCAGTCCAAGACTAA 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATCATCTATTGCCTGAGAGCACAGCAGGAGGACAATGATGGTCGGGATATAAACCCAAGTC
                                                                                  ANCTIGGGAAGGTGACCGCATCTTTAAACATGGGGCTTGCAACTTAGGTCACACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC
  AATTTGAGATCGAATATAATGTAGAGCAGAGCCTTCAAAACACTGCACCCTGGGGGCCT
                                                                                                                                                                                                                                                                                                                                         592 GCTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCTTCCAGAAT
                                                                                                                                                                                                                                                                                                                                                                              TGAAGCTGTAAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATCTACCGCAGACCCCTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 TGGGGACTGAGAACAGGACTAGCTGGATTTCYTAGGCTGACTAAGAATCCCTAAGCT
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                                                              AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA
                                                                                                                                                                               AATTCGAGATCGAATACAACGTAGAGCAGAGGAGCTTCGAAACACTGGACCCTGGGGCCT
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleo Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1019)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30771765.
                                                                                                                                                                                                                                                                                                 TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGT
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BX439636 Homo sapiens PLACENTA Homo 3-PRIME, mRNA sequence.
BX439636
BX439636.2 GI:47000005
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
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                                                                                                                                                                                                                                                                                                                         530 CGAAGCTGTAAAACTA-------CAAATGGAGCCCARGATGCAGTCCARGACTAG 483
                                                                                                                                                                                                                                                                                                                                                                                                                  #82 GDTCTACCGCGGCCCCCTGGACCGGCCTGCTSGCCCCCGMTCTGATGTTAATGACATCAA 423
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BX357208 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI022YJ18 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 ANCTGGGAAGGTGACCGCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCG 660
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Li (bases I to 788)
Li (M.B., Gruber, C., Jessee, J. and Polayes, D.
Full-Length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30376125.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                              AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGGCCT
                                                            AATTCGAGATCGAATACAACGTAGAGCAGAGGAGCTTCGAAACACTGGACCCTGGGCCT
                                                                                                                  CCTCAGCCAATGGATGCCCTGGACTCTCCCCCTTAGGACCTCTAGCAGCTATAATATT
                                                                                                                                                 CCTCAGCCAATGGATGCCCTGGATTCTCCCCCTTCTTAGGACCTCTAGCAGCTATAATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 TGGGGGACTGAGAGACMGGACTGGCTGGATTTCCTAGGCTGACTAAGAATCCCTARGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AATCTACCGTGGACCCCTGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCGCCGCCCCCCCCTTTGGGTCCCCTTTCGTNNTGGGAGCTCTGT
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Homo sapiens
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BX357208/c
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st srrand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecox V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 28-APR-2004
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                                            ACCAATCAGAGAGCTCACTAAAATGCTAAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC 720
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CENTA COT 25-NORMALIZED Homo sapiens cDNA
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                   AATCATCTATTGCCTGAGAGCACAGGAAAGGACAAGGATTGGGATATAAACTCAGGCA
                                                                                                                                                                                                                                                     TTCGAGCCGGCAACAGAAACCYYYTTT-TTTCYCYCYCTTTTTGTNTGGGNDTTTTTTTT
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Matches 693; Conser
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BX380176/c
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1...771
| organisme="Homo sapiens"
| organisme="Homo sapiens"
| db xref="taxon:9606"
| clone="IMAGE:4993894"
| clone="MGG36"
| lab host="H108"
| lab host="H108"
| note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
                                                                                                                                                      BIO87886 171 bp mRNA linear EST 20-JUN-2001
602852690F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4993894 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGACCCTGGGGCCTCCTCAGCCAATGGATGCCCTGGATTCTCCCCCTTCTTAGGACCTCTA 120
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 771)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 762.
High quality sequence stop: 762.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 44.7%; Score 593.4; DB 4; Best Local Similarity 89.2%; Pred. No. 2.2e-168; Matches 688; Conservative 0; Mismatches 68;
                                  16
       50 GGCMACCCCCYCTGGGTCCCCTTCCTTTGTATGGG
                                                                                                                                                                                                                                                 BI087886.1 GI:14506216
                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                mRNA sequence.
BI087886
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                       RESULT 12
BI087886
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SOURCE
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                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIOZYUJ8"
/tissue type="PlaCENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4215.r.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                     For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI022DE09NP1&c=4215.r. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 758;
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Pred. No. 6.9e-173;
9; Mismatches 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 gegacaardarcaegararaaacceaegearreaaeceaegeaegecaegeraecereirreeg 1303
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                                                                                                           Shiraki
                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 73 Row: k Column: 22
This clone has the following problem: retained intron.

Location/Qualifiers
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: capaba-remail.nih.gov
Tissue Procurement: Milos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shira
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G. B. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
contact: amadanadsystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 ACTACACTCCAATTCAGTAGGAAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 520 ACTIGGGTTTTCCTGTTGAGAGGGTGGACTGAGACAGGACTAGCTGGATTTCCTAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 TGACTAAGAATCCCNAAGCCTANCTGGGAAGGTGACCGCATCCATCTTTAAACATGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  691 CAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATCTATTGCCTGAGAGCACAGGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.4204,
/organism="Homo sapiens"
/mol_trype="mRNA"
/db_xref="teaxon:9606"
/clone="IMAGE:5265109"
/clone lib="NH MGC 95"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Vector: pBluescript"
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G. Klausner, R.D., Collins, F.S., Wagner, L., Scheafer, C.M., Schuler, G.D.,
Klausner, R.D., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkerman, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterffeld, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Length
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4204)
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Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                                                              CCCAATTCAGCAGGAAGCAGTTAGAGCGGTCGTC-GGCAAACCTCCCCAAAAGCACTTAGG
                                                                                                                                                                            TTTTCCTGTGTGAGATGGGGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTA
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                                     TCCAATTCAGTAGGAAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGG
                                                                                                                                         TTTTCCTGT-TGAGAGGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTA
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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454

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

12. (bases 1 to 900)

13. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

14. Pull-length cDNA libraries and normalization

15. Unpublished (2001)

16. May 22, 2003 this sequence version replaced gi:31021096.

17. Contact: Genoscope

18. Genoscope - Centre National de Sequencage

18. BP 191 91006 EVRY cedex - France

18. Bmail: seqref@genoscope.cns.fr

18. Bmail: seqref@genoscope.cns.fr

18. strand cDNA was primed with a Not1-oligo(dT) primer. Five prime

18. end enriched, double-strand cDNA was digested with Not I and cloned

18. into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX459153 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE013YI20 3-PRIME, mRNA sequence.
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                                                                                     121 TIAGGACCTCTAGCAGCTATAATATTGCTACTCCTCTTTGGACCCTGTATCTTTAACCTC 180
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491 GGGGCTTGCAACTTAGCTCACACCTGACCAATCAGAGAGCTCACTAAAATGCTAATTAGG
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                                                                                                                                   275 CTTGTTAAGTTTGTCTTCCAGAATTGAAGCTGTAAAAGCTACAAATAGTTCTTCAAATG
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Homo sapiens
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BX459153/c
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DEFINITION
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VERSION
KEYWORDS
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ORGANISM
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AUTHORS
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/mol_type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENEU"
/note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
                                                                                                                                                                                                                       TCACTGGGTTCCATGGTTCTCTTCCATGACCCACGGCTTCTAATAGAGCTATAACACTCA 1170
                                                                                                                                                     CCGCATGGCCCAAGATTCCATTCCTTGGTATCTGTGAGGCCAAGAACCCCAGGTCAGAGA 1230
                                                                                                                                                                                                                                                                     ANGTGAGGCTTGCCACCATTTGGGAAGTGGCCCACTGCCATTTTGGTAGCGGCCCACCAC 1290
                                                                                                                                                                                                                                                                                          EST 16-MAY-2004
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1 (bases 1 to 719)

1 Enadenberger, N., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,

Lebkowski, J. and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that control human Es cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Regenerative Medicine
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                                                                 CTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAATAGAACTGAACACTGG
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CN272394
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85.4%; Pred. No. 1.5e-158;
tive 0; Mismatches 62; Indels 5
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                                                                                                                                                                                                                                                                                                                                      CATCTTGGGAGCTGTGGGAGCAAGGATCCCC 1321
                                                                                                                                                                                                                                                                                                                                                       Email: rbrandenberger@geron.com
Insert Length: 719 Std Error: 0.00.
Location/Qualifiers
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230 Constitution Drive, Menlo Park,
TTE1: 650 473 8658
Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN272394.1 GI:47288808
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Homo sapiens
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Matches 657,
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CN272394
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DEFINITION
ACCESSION
VERSION
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ORGANISM
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BX953822 1002 bp mRNA linear EST 01-MAR-2004 DKFZp781M064 r1 781 (synonym: hlcc4) Homo sapiens cDNA clone DKFZp781M064 5', mRNA sequence.
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/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="mrgrap="adult"
/lab host="DH108"
/clone="lib="781 (synonym: hlcc4)"
/note="vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB; cDNA-collection"
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BST (Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., et al.)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email 8. Wiemann@dKz- heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        German Genome Project.

No s1 sequence available.
This clone (DKF2p781M064) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        669 GAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATCT
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1. (Dases 1 to 1002)
Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager,
Mewes, H.W., Weil, B., Amid, C., Osanger, A., Pobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
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Pred. No. 3.8e-140;
0; Mismatches 72;
                                                                         814
                                                                                                 BCCGCGCGGCTACGCCCCCCTKTGGTCCCC
                                                                                                                                                                                                                                                                                                               BX953822
BX953822.1 GI:43433374
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al Similarity 87.6%;
641; Conservative
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                                                                                                                                                                                  /mol_type="mRNA"
//mol_type="mRNA"
//mol_type="mRNA"
/clone="CSODE013Y120"
/tissue_type="PLACENTA"
/clone=lib="Homo saphens FIRACENTA"
/note="Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, wouth a NotI-oligo(dT) sprimer. Five prime end enriched, the NotI and ECCRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                 division of Invitrogen.
This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE013BE10NP1&c=4215.r.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.9%; Score 544; DB 5; Length 900; 77.5%; Pred. No. 2.4e-153; ive 49; Mismatches 120; Indels
normalized. Library was constructed by Life
                                                                                                                                                                 organism="Homo sapiens"
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

Direct Submission

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1.7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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                                                                                                                                                                                                                                                          TIGICCTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTCTTCCATGACCCACG 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGI13694 679 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-120G11.R, genomic survey sequence.
AG113694
                                                                                                                                                 TCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGTA-CCCAT 1026
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Pan troglodytes
Eukaryota / Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Pan.
TGCCACTCCCGATCAGGCTAAAGGCTTGCCA-TTGTTCCTGCATGGCTAAGTGCCTGGGT
                                                                                                                                                                                                                                                                                                                              GAGCTTTTGTTCGCCATCCACCACTGCTGTT-TGCCACCGTCACAGACCCGCTGCTGACT
                                                                                                                        GAGCTTTCGCTCACTGTCCACCACTGCTGTTTTGCCGCCGTAGCAGACTCGCTGCTGACT
                                         TTCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTATGGCTCAAGCT
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BAC end sequences of Library PTB
Unpublished
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 GTAATGGAGCTGAACACTAGTCGCTGAGTTCCACAGTTCTCTTCCGTGACCCACGGCTTG
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                                                                                                                                                                                                                                                                                                                     678 GCTCGGTAAGATGCTAATAAGGCAAAAAACAGGAGGTAAAGAAAATAGCCAATCTATTG
                                                                                                                                                                                                                                                                                                                                                                                     733 CCTGAGAGCACAGGGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAGCCAGCA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                       5;
                                                                                                                                                                                               619;
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="pTB=120G11.R"
/sex="male"
/cell_type="lymphoblast"
/cell_type="lymphoblast"
                                                                                                                                                                                               Length
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                                                                                                                                                                                          Query Match 36.2%; Score 480.8; DB 9; Best Local Similarity 86.7%; Pred. No. 3.5e-134; Matches 552; Conservative 0; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 TTTTGGAAGTGGCCCGCCACCATCTTGGGAGCTCTCG
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Homo sapiens
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Pred. No. 1.8e-132;
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89.6%; Pred. No. ...
... 0; Mismatches
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                  1254 GAAGTGGCCCACTGCCATTTTGGTAGC 1280
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                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol type="mxnx"
/mol type="mxnx"
/db_xref="taxon:9606"
/dlone="taxon:9606"
/clone="taxon:9606"
/clone="taxon:9606"
/clone="taxon:10"
/lab host="DH10B"
/clone="taxon:10"
/note="Organ: pooled pancreas and spleen; Vector:
pCWV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is destroyed upon cloning). Average insert
size 1:5 kb, insert size range 1-2:5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1014 GCGAGGTACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCT 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1074 AAGTGCCTGGGTTTTGTCCTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTCTT 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCCGCTGCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCA 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAGAGACAGGACTAGCTGGGATTTCTAAGGCGGACTAAGAATCCCTAGGCCTAGTTAGG 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-----AGAGAGCTCACTAAAATGCTAATCAGGC-AAAAACAGGAGGTAAAGCAAT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCCAATCATCTATTGCCTGAGAGCACAGCGGGAAGGACAAGGATTGGGATATAAACTCA 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCATTCAAGCCAACAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTG 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTATGGCTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAG 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTACCGCTCAAGCTAAGCTTTCGCTCGTTGTCCACTGCTGTTTGCCGCAGTCGCAG 467
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.lln.gov
Plate: LiAM12773 row: b column: 09
High quality sequence stop: 685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGTGACCGCATCCACCTTAAACCATGGGGCTTGCAACTTAGCTCACACCCGACCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 480.8; DB 4; Length 999;
Pred. No. 4e-134;
0; Mismatches 110; Indels 16
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83.1%;
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Best Local 9
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Matches
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        COMMENT
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submitssion
and Chemical Research (RIKBN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the RkD process and may have higher chance of
1193
                                                                                                                        CTTGGTATCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGG 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS 04-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
                                                                                                                                                                227 CITGGAATCCGTGGGGCCAAGAACCCCAGGTCAGAGAACGAGAGGGGTTGCTGCTGCCATCTTG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           845
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AG134524 683 bp DNA linear GSS 04-NOV-200
Pan troglodytes DNA, clone: PTB-147110.R, genomic survey sequence.
AG134524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
CCATGACCCACGCCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTC
                                    58 TCGNAGAGCTCACTAAAATGCTAATTAGGCAAAAAACAGGAGGTAAAGAAATAGCCAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   726 TCTATTGCCTGAGAGCACAGCGGGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taylor, T.D., Yada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
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/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Gaps

728

168

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Fartroglodytes DNA, clone: PTB-124K18.F, genomic survey sequence. AG116971.7490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   967 TICCAICCCITIGGAICCAGCAGAGIGICCACIGIGCICCIGAICCAGCGAGGIACCCAT 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTATCTGTG 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1207 AGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGGGAAGTGGCCCACT 1266
                                                                                                                                                                                                                                         49 GAGAGCTCACTAAAATGCTGATTAGGCAAAAAGCAGGAGGTAAAGAAATAGCCAATCATCT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           789 AGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTCACTCTAT 848
                                                                                                                                                                                                                                                                                              729 ATTGCCTGAGAGCACAGGGGAAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAGCC 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519 CTTCTAATAGAGCTATAACACTCACCGCATGGCCCCAAGATTCCATTGCATTGGAATCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 GTGAGCTTTTGATTGCCGTCCACCAGTGCTGTTTGCTGCCGCCGACCACCGCCGCGCGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459 CGTCCTAATCGAGCTGAACACTAGTCATGGGTTCCATGGTTCTCTTCCGTGACTCCATGG
                                                                                                                                                                                                                    669 GAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATCT
                                                                                                                                                                                                                                                                                                                       169 GGCAACGCCTACCTTTGGGTCCCCTTTGTATGAGAGCTCTGT-----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 TICACTCTATTAAAICTTGCAACTGCACTCTTTATGTTCCATGTTTGTTACAGCTCGAG
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BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                              12;
/db_xref="taxon:9598"
/clone="PTB-030D19.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                       Length 669;
                                                                                                                      Score 474; DB 9; Lengtn oo. Pred. No. 4.1e-132;
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                                                                                                                                                                              0; Mismatches
                                                                                                                                       35.7%;
il Similarity 86.8%;
548; Conservative
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                                                                                                                                       Query Match
Best Local Similarity
Matches 548; Conserv
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AG116971
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:s181-45-503-9111, Pax:81-445-503-9170)
Telsial-45-503-9111, Pax:81-45-503-9170)
Telsial-46-from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                    ACTICCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGTACCC 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                       1145 GGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCCAAGATTCCATTCCT-TGGTATCT 1203
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                                                                                                                                                                                                                                                                                ATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATGTTCCTGCATGGCTAAGTGCCTGGG 1084
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                                                                                                                                                                                                                                                                                                    ATTGCCGCTCCTGATCGGGCTAAAGGCTTGCCATTCTTCCTGCACGGCTAAGTGCCTGTG 476
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                                                                                                                                                           GCTGAGCTTTCTCTCGCCATCCACCACTGCTGTTTTGCCGCCGTCGCAGACCGGCCGCTG 356
    236
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Pan troglodytes DNA, clone: PTB-030D19.F, genomic survey sequence.
AG049953
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                         357 ACTICCATCCCTCCAGATCCAGCAGGGTGTCCGCTGTGCTCCTGATCCAGCGAGGCGCCC
    GCCAGCAACGCCAACCCCCTTTGGGT-CCCTCCCCTTGTATGGGAGCTCTGTTTTCACTC
                                                               237 TATTTCACTCTATTAAATCTTGCAACTGCACTCTTCTGGTCCGGTTGTTGTTACGGCTCGA
                                                                                                                      GCTGAGCTTTTGTTCGCCATCCACCACTGCTG-TTTGCCACCGTCACAGACCCGCTGCTG
                                             TATTICACICIATIAAAICAIGCAACIGCACTCTICIGGICCGIGITITITAIGGCICAA
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/wol_type="genomic DNA"
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
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R.Site 1 : SacI
R.Site 2 : SacI.
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Tothiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Tothiyama, A., Hattori, M., Watanbe, H. and Sakaki, Y.
Tothi, Y., Watanbe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
In 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Clnss are derived from the chimpanzee BAC library PTB This BAC end close are derived from the chimpanzee BAC library PTB This BAC end close tracking errors.
                                                                                                                      AG096341 710 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-097K23.F, genomic survey sequence.
AG096341
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                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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85.1%; Pred. No. 9e-131;
ive 0; Mismatches 65;
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                        RESULT 22
                                                                                                             AG096341
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                                                          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
/mol_type="genomic DNA"
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/cell_type="lymphoblast"
/cell_type="lymphoblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.6%; Score 473; DB 9; Length 681; larity 88.8%; Pred. No. 8.2e-132; Conservative 0; Mismatches 56; Indels 3
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                           Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
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Best Local S:
Matches 538
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                                        TITLE
JOURNAL
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site:

http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Bickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,

R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    997 CACAGCAGGAGGGACAATGATCGGGATATAAACCCAAGTCTTCGAGCCGGCAACGGCAAC
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AGENCOURT_7917208 NIH_MGC_72 Homo sapiens CDNA clone IMAGE:6161436
                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 41 Row: m Column: 10 This clone has the following problem: retained intron. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   877 CCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTGACCAATCAGAGAGGTCACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 ACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGAAGTCACCCCTCCCGAGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 468.2; DB 3;
Pred. No. 2.8e-130;
0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .1160
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/tissue_type="Placenta"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="Vector: pDNR-LIB"
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Best Local Similarity 90.1%;
Matches 500; Conservative
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BQ437925
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Klausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausher, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Hellcon, E., Ketteman, M., Madan, A., Poung, A.C., Shevchenko, Y.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.W.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jonee, S.J. and Marra, M.B.
                                                                                                                                                                                                                                                                                          1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC030968 1160 bp mRNA linear HTC 19-NOV-2003 Homo sapiens cDNA clone IMAGE:4724433, with apparent retained
                                                                                                                                                                                                                                                                                                                                                                                                                           TAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTATCTGTGAGGC 1210
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1160)
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                                                                                                                                                                                         425 GCTCCCGATCGGGCTAAAGGCTTGCCATTGTTCTTCTGCACGGCTAAGTGCCTGGGTTCGTC
                                                                                                                                                                                                                                                                                                                          TAATAGAGCTATAACACTCACCGCATGGCCCCAAGATTCCATTGGAATCCGTGAGGC
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22388257
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tisgue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
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Homo sapiens
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Direct Submission
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BC030968
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1177 GGCCCAAGATTCCATTCCTTGGTATCTGTGAGGCCAAGAACCCCCAGGTCAGAGAANGTGA 1236
                                                                                                                                                                                                                                                                                                                 1237 GGCTTGCCACCATTTGGGAAGTGGCCCACTGCCATTTTGGTAGCGGCCCACCACCATCTT 1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, Wir.http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-85-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                          625 GACTTGCCACCATCTGGAAGTGGCCGTCACCATCTTGGAAGCGACCTGCCACCATCTT 684
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Pan troglodytes DNA, clone: PTB-064H14.R, genomic survey sequence.
AG072852
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Ban troglodytes
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidee; Pan.
                                                               445 CTIGITICCIGCAGGCCTAAGTGCCCAGGTTCGTCCTAATCTAGCTAAACACTAGTCACTG
                                                                                                                                                         GGTTCCACGATTCTCTTCCATGACCCACAGCTTCTAATAGAGCTATAACACTCGCCGCTT
                                                                                                                                                                                                                                                           1057 ATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAATAGAACTGAACACTGGTCACTG
                                                                                                                                 GGTTCCATGGTTCTTCCATGACCCACGGCTTCTAATAGAGCTATAACACTCACCGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fullyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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86.4%; Pred. No. 1e-126;
ive 0; Mismatches 74; Indels 9
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/clone_lib="PTB Chimpanzee Male BAC Library'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .670
/organism="Pan troglodytes"
/mol type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB=064H14.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                             1297 GGGAGCTGTGGGAGCAAGGATCCCC 1321
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Best Local Similarity 86.4
Matches 529; Conservative
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R.Site 2
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                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (Bases I to 893)

I (Bases I to 893)

NIH-MGC http://mgc.nci.nih.gov/.

I unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTP/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 650.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="INAGE:61436"
/tissue type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="WIH MGC 72"
/note="Organ: skin; vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               697 AAAACAGGAGGTAAAGCAATAGCCAATCATCTATTGCCTGAGAGCACAGGGGAAGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      757 AGGATTGGGATATAAACTCAGGCATTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCT
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Best Local Similarity 80.4%; Pred. No. 2.1e-129;
Matches 599; Conservative 0; Mismatches 101; Indels 45; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
5', mRNA sequence.
BQ437925
BQ437925.1 GI:21177001
                                                                                            Homo sapiens (human)
                                                                                                                       Homo sapiens
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Pan troglodytes DNA, clone: PTB-130M15.F, genomic survey sequence. AG121669.
AG121669.
AG121669.1 GI:16650834
GSS.
Pan troglodytes (chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                          671 GAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 GAGCTCACTAAAATGCTAATTA-GCAAAAACAGGAGGTAAAGAAATAGCCAATCATAT
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                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                               9.
                                                                                                                                                       /mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB=102B07.F"
/sex=male="Yppe="lymphoblast"
/cell_type="lymphoblast"
/cell_type="lymphoblast"
                                                                                                                                                                                                                                                                                                                                                 712;
                                                                                                                                                                                                                                                                                                                                            Score 455; DB 9; Length 71
Pred. No. 2.5e-126;
0; Mismatches 76; Indels
                                                                                                       1.712
/organism="Pan troglodytes"
                          tor : pKS145
ite 1 : SacI
ite 2 : SacI.
Location/Qualifiers
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Best Local Similarity 86.2%;
Matches 529; Conservative
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Totoki, Y., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (O2-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170,
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                     1028
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Pan troglodytes DNA, clone: PTB-102B07.F, genomic survey sequence.
AG099717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes (chimpanzee)
Ban troglodytes
Eukaryots offetacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                       AGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTCACTCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGTACCCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 CCACTCCTGATCGGGCTAAAGGCTTGCCATTGTTCCTGCACGGTTAAGTGCCTGGGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTTCCATGACCCACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468 TCCTAATCGAGGTGAACACTAGTCACTGGGTTCCACGGTTCTCTTCCATGACCCACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTATCTGTGAG
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GAGAGCTCACTAAAAAGCTAATTAGGCAAAAACAGGAGGTAAAAGAAATAGCCAATCATTT
                                                                                                                                                                                  AGCAACGGCTACCCTCTTTGGGTTCCCTCCTTTGTATGGGAGCTCTTTTTTCACTCTAT
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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RESULT 26
AG099717
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SOURCE
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REFERENCE AUTHORS

JOURNAL REFERENCE AUTHORS

TITLE

TITLE JOURNAL

COMMENT

577

1030

457

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730 165 850

284

790 225 910

337 970 397 1210

1270

697

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/downer lib="Entamoba histolytica Sheared DNA"
/downer lib="Entamoba histolytica Sheared DNA"
/note="Vector: pHOS1; Sire 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, U.S. (1993) Entamoba histolytica: method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Vener, J.C. (Making small insert libraries for
                                                                                                                                                                                                                  BH149565 921 bp DNA linear GSS 27-AUG-2001
ENTQG48TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                      Entamocba histolytica

Eukaryota; Entamocbidae; Entamocba.

Eukaryota; Entamocbidae; Entamocba.

E 1 (Dases 1 to 921)

S Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamocba histolytica

HM1: IMSS sheared DNA library (2001)

Unpublished (2001)

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: bjlottuseligr.org
    TATTGCCTGAGAGTACAGCGGGAAGGACAATGATCGGGATATAAACTCATGCATTCGAG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-----AGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGGGGTAAAGCAATA 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 ACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               607 GAAGGIGACCGCATCCATCITIAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84; Indels
                                                                     CCAGCAACAGCAACCCCTTTGGGTCCCCTCCCATTGTATGGG 829
                                                                                                              84
                                                                                               CCACCAATGGCTACCCTCTTTGGGTCCCCTCCCTTTGTTATGG

    . 921
    /organism="Entamoeba histolytica"

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Pred. No. 2.3e-121;
0; Mismatches 84;
                                                                                                                                                                                                                                                  genomic, genomic survey sequence. BH149565
BH149565.1 GI:15310303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
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High quality sequence stop: 567.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                           Entamoeba histolytica
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Best Local Similarity 83.8
Matches 550; Conservative
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                            186
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                                                                                                                                                            Totoki,Y., Wattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Direct Submission

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbesdsgs.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Clones are derived from the chimpanzee BAC library PTB This BAC end

was generated during the R&D process and may have higher chance of
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Eukaryota, Metazoa; Chordata; Craníata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                 Taylor, T.D., Yada, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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Pred. No. 1.6e-121;
0; Mismatches 66;
                                                            Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library PTB Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .689
/organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="PTB-130M15.F"
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87.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-M0G-2001) Asao Pujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                 CCGCTGCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGC 1015
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CAGGTAGTAAAGAGGCTCACTAAAACGCTAATTAGGCAAAAACAGGAGGTAAAGAAATA 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                            182 GAGGCACCCATTGCCGCTCTGGATTGGGCTAAAGTCTTGTCATTGTTCTTGCACGCTAA 123
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Pan troglodytes DNA, clone: PTB-071A23.R, genomic survey sequence.
AG076758
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                         GCCAATCATCTATCGCCTGAGAGACACACTGGGAGGACAATGA-TAGGATATAAACCCAG
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                                      GCCAATCATCTATTGCCTGAGAGCACAGCGGAAGGACAAGGATTGGGATATAAACTCAG
                                                                                                                                                                                  838 TITCACTCTATITCACTCTATIAAAICAIGCAACTG - CACTCTICTGGTCCGTGTTTT
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Direct Submission
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/mol_type="genomic DNA"
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
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1. .679
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Pan troglodytes DNA, clone: PTB-106G16.F, genomic survey sequence.
AG102951.1 GI:16723468
GSS.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fullyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
Submitted (02-AUG-2001) Asao Fullyama, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 GATGCCCTGGCCCCTTCTTAGAACCTGTAGCAGCTGTAAGGCTGTTGCTCCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 AGACAGGACTAGCTGGGATTTCCTAGACCGACTAAGAATCCCTAAGCCTGGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 AATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGCCTCCTCAGCCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 TGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAATTGAAGCTGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 GCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAAAATCTACCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 GCTACAAATGGTTCTTCAAATGAAGCCCCAGATGCAGTCCATGGCTAAAAATCTACCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 ACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGAAGTCACCCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433 CGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGGAAGCAGTTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 TGAGGAAATCTCAACTGCACAACCCCTACCATGCCCCATTTCAGCAGGAAGCAGGTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            493 CAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTTCCTGTTGAGAGGGTGGACTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCACCTATAATATTTTTACTCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553 AGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGGGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                              BAC Library
                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                  32.8%; Score 435.6; DB 9;
86.3%; Pred. No. 1.9e-120;
cive 0; Mismatches 76;
                                                                                                                                                                                                   Chimpanzee Male
/db_xref="taxon:9598"
/clone="PTB-071A23.R"
/esc="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               673 GCTCACTAAAATGCTA 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 GCTCTCGAGCATGCTA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 683)
                                                                                                                                                                                                                                                                                                                                       Query Match 32.8
Best Local Similarity 86.3
Matches 480; Conservative
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1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1026 TTGCCACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGT 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGTACCCA 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTICACICIATIAAAICAIGCAACIGCACTCTICIGGICCGIGITTITIAIGGCICAAG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arricacrcratiaaarcrigcaacrgrgcrcritcrggrccgrgrirgraarggcrcaag 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   547 ACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGG 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTATTGCCTGAGAGGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTTGAG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              607 GAAGGIGACCGCAICCAICITIAAACAIGGGGCIIGCAACIIAGCICACACCCGACCAAI 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccecchacccccarricgcrcccrccc--rrenardcchacrcrcrrrrrcacrcr 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTATTGCCTGAGAGCACAGGGGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCAACAGCAACCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 683;
                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1086 TIGICCIAATAGAACIGAACACIGGICACIGGGIICCAIG 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    644 TCATCCTAATCGAGCTGAACACTAGTCACTGTGTTCCAGG 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 433.6; DB 9;
Pred. No. 7.8e-120;
0; Mismatches 61;
                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 683
(organism="Pen troglodytes"
(db Aref="taxon:9598"
(clone="PTB-106G16.F"
                                                                                                                                                                                                                            Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                                                               Sequencing: -21M13
LIBRARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             514; Conservative
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Best Local Similarity
Matches 514; Conserva
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                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                           COMMENT
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Search completed: January 22, 2005, 19:31:51 Job time : 3968.84 secs